

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Daggett, Lorrie P.  
Ellis, Steven B.  
Liaw, Chen W.  
Lu, Chin-Chun
- (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
SUBUNITS, DNA ENCODING SAME AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
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  - (C) CITY: Los Angeles
  - (D) STATE: CA
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 90071-2921
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 20-APR-1994
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/052,449
  - (B) FILING DATE: 20-APR-1993
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Reiter, Stephen E.
  - (B) REGISTRATION NUMBER: 31,192
  - (C) REFERENCE/DOCKET NUMBER: P41 9424
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 619-546-4737
  - (B) TELEFAX: 619-546-9392

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4298 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 262..3078

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCCGAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
60	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
75	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
95	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
110	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
125	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
140	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
155	
CAC GAG GGC CCG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	185
175	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	200
190	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	215
205	
210	

ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220 225 230	963
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly 235 240 245 250	1011
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile 255 260 265	1059
CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser 270 275 280	1107
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys 285 290 295	1155
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile 300 305 310	1203
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr 315 320 325 330	1251
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg 335 340 345	1299
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val 350 355 360	1347
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys 365 370 375	1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met 380 385 390	1443
TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr 395 400 405 410	1491
GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val 415 420 425	1539
AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr 430 435 440	1587
TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe 445 450 455	1635
TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr 460 465 470	1683
GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val 475 480 485 490	1731

AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu 495 500 505	1779
AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu 510 515 520	1827
CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu 525 530 535	1875
ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe 540 545 550	1923
ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val 555 560 565 570	1971
CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe 575 580 585	2019
GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAG GAC GCA CTG ACC Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr 590 595 600	2067
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly 605 610 615	2115
ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met 620 625 630	2163
GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn 635 640 645 650	2211
CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly 655 660 665	2259
ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala 670 675 680	2307
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu 685 690 695	2355
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala 700 705 710	2403
GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile 715 720 725 730	2451
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu 735 740 745	2499
GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2547

CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2595
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 795 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg 895 900 905	2979
GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile 910 915 920	3027
GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser 925 930 935	3075
TGAGACTCCC CGCCCCCCTT CCTCTGCCCC CTCCCCCGCA GACAGACAGA CAGACGGACG	3135
GGACAGCGGC CCGGCCACG CAGAGCCCCG GAGCACCACG GGGTCGGGGG AGGAGCACCC	3195
CCAGCCTCCC CCAGGCTGCG CCTGCCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC	3255
GTCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTTCT	3315
ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCGC TCAACCTCTC AGATCCCTCG	3375
GTCAGCACCG TGGTGTGAGG CCCCCGAGG CGCCACCTG CCCAGTTAGC CCGGCCAAGG	3435
AACTGATGG GTCCTGCTGC TCGGAAGGC CTGAGGGAAG CCCACCCGCC CCAGAGACTG	3495
CCCACCCTGG GCCTCCCGTC CGTCCGCCCG CCCACCCCGC TGCCTGGCGG GCAGCCCCTG	3555
CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGGCAG	3615
GGCCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG	3675
GCTAACTGCC CCCAGGCGGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC CTTCCCGCAG	3735
CACCAGCCTG AGCCACAGTG GGGCCCATGG CCCCAGCTGG CTGGGTCGCC CCTCCTCGGG	3795

CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCCTC TTCTTGCGGC ACCGCCCACC 3855  
 AAACACCCCG TCTGCCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT CCCCCACGGC 3915  
 CGTCCCTGAC TTCCAGCTG GCAGCGCCTC CCGCCGCCTC GGGCCGCCTC CTCCAGAATC 3975  
 GAGAGGGCTG AGCCCCCTCT CTCCTCGTCC GGCCTGCAGC ACAGAAGGGG GCCTCCCCGG 4035  
 GGGTCCCCGG ACGTGGCTC GGGACTGTCT TCAACCCTGC CCTGCACCTT GGGCACGGGA 4095  
 GAGCGCCACC CGCCGCCCC CGCCCTCGCT CCGGGTGCGT GACCGGCCCC CCACCTTGTA 4155  
 CAGAACCAGC ACTCCCAGGG CCCGAGCGCG TGCCTTCCCC GTGCGCAGCC GCGCTCTGCC 4215  
 CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCCAACCCCC ACCTCCCGGT GTATGCAGTG 4275  
 GTGATGCCTA AAGGAATGTC ACG 4298

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 938 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser  
 1 5 10 15  
 Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val  
 20 25 30  
 Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln  
 35 40 45  
 Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser  
 50 55 60  
 Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu  
 65 70 75 80  
 Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro  
 85 90 95  
 Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly  
 100 105 110  
 Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr  
 115 120 125  
 Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr  
 130 135 140  
 Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp  
 145 150 155 160  
 Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala  
 165 170 175  
 Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu  
 180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu  
 195 200 205  
 Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser  
 210 215 220  
 Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met  
 225 230 235 240  
 GlyThr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser  
 245 250 255  
 Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile  
 260 265 270  
 Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val  
 275 280 285  
 Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro  
 290 295 300  
 Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu  
 305 310 315 320  
 Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly  
 325 330 335  
 Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser  
 340 345 350  
 Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn  
 355 360 365  
 Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly  
 370 375 380  
 Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile  
 385 390 395 400  
 Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser  
 405 410 415  
 Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys  
 420 425 430  
 Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg  
 435 440 445  
 His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile  
 450 455 460  
 Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala  
 465 470 475 480  
 Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys  
 485 490 495  
 Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met  
 500 505 510  
 Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu  
 515 520 525  
 Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys  
 530 535 540

Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser  
 545 550 555 560  
 Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met  
 565 570 575  
 Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn  
 580 585 590  
 Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp  
 595 600 605  
 Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro  
 610 615 620  
 Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala  
 625 630 635 640  
 Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val  
 645 650 655  
 Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu  
 660 665 670  
 Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser  
 675 680 685  
 Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg  
 690 695 700  
 His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala  
 705 710 715 720  
 Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu  
 725 730 735  
 Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu  
 740 745 750  
 Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp  
 755 760 765  
 Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe  
 770 775 780  
 Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser  
 785 790 795 800  
 Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val  
 805 810 815  
 Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe  
 820 825 830  
 Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met  
 835 840 845  
 Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp  
 850 855 860  
 Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe  
 865 870 875 880  
 Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser  
 885 890 895



Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn Gln  
 900 905 910

Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln  
 915 920 925

Leu Gln Leu Cys Ser Arg His Arg Glu Ser  
 930 935

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	TCC	TAT	GAC	AAC	48
Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	
1				5				10						15		

AAG	CGC	GGA	CCC	AAG												63
Lys	Arg	Gly	Pro	Lys												
			20													

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	
1				5				10						15		

Lys	Arg	Gly	Pro	Lys												
			20													

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 189..3899

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCTTAATAA GATTTGCCAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA	806
Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	
195 200 205	

GGG Gly	CCG Pro	CGC Arg	GCG Ala	CGC Arg	ACG Thr	CAG Gln	CGC Arg	CTG Leu	CTG Leu	CGC Arg	CAG Gln	CTC Leu	GAC Asp	GCG Ala	CCC Pro	854
			210					215					220			
GTG Val	TTT Phe	GTG Val	GCC Ala	TAC Tyr	TGC Cys	TCG Ser	CGC Arg	GAG Glu	GAG Glu	GCC Ala	GAG Glu	GTG Val	CTC Leu	TTC Phe	GCC Ala	902
		225					230					235				
GAG Glu	GCG Ala	GCG Ala	CAG Gln	GCC Ala	GGT Gly	CTG Leu	GTG Val	GGG Gly	CCC Pro	GGC Gly	CAC His	GTG Val	TGG Trp	CTG Leu	GTG Val	950
	240					245					250					
CCC Pro	AAC Asn	CTG Leu	GCG Ala	CTG Leu	GGC Gly	AGC Ser	ACC Thr	GAT Asp	GCG Ala	CCC Pro	CCC Pro	GCC Ala	ACC Thr	TTC Phe	CCC Pro	998
255					260					265					270	
GTG Val	GGC Gly	CTC Leu	ATC Ile	AGC Ser	GTC Val	GTC Val	ACC Thr	GAG Glu	AGC Ser	TGG Trp	CGC Arg	CTC Leu	AGC Ser	CTG Leu	CGC Arg	1046
				275					280					285		
CAG Gln	AAG Lys	GTG Val	CGC Arg	GAC Asp	GGC Gly	GTG Val	GCC Ala	ATT Ile	CTG Leu	GCC Ala	CTG Leu	GGC Gly	GCC Ala	CAC His	AGC Ser	1094
			290					295					300			
TAC Tyr	TGG Trp	CGC Arg	CAG Gln	CAT His	GGA Gly	ACC Thr	CTG Leu	CCA Pro	GCC Ala	CCG Pro	GCC Ala	GGG Gly	GAC Asp	TGC Cys	CGT Arg	1142
		305					310					315				
GTT Val	CAC His	CCT Pro	GGG Gly	CCC Pro	GTC Val	AGC Ser	CCT Pro	GCC Ala	CGG Arg	GAG Glu	GCC Ala	TTC Phe	TAC Tyr	AGG Arg	CAC His	1190
	320					325					330					
CTA Leu	CTG Leu	AAT Asn	GTC Val	ACC Thr	TGG Trp	GAG Glu	GGC Gly	CGA Arg	GAC Asp	TTC Phe	TCC Ser	TTC Phe	AGC Ser	CCT Pro	GGT Gly	1238
335					340					345					350	
GGG Gly	TAC Tyr	CTG Leu	GTC Val	CAG Gln	CCC Pro	ACC Thr	ATG Met	GTG Val	GTG Val	ATC Ile	GCC Ala	CTC Leu	AAC Asn	CGG Arg	CAC His	1286
				355					360					365		
CGC Arg	CTC Leu	TGG Trp	GAG Glu	ATG Met	GTG Val	GGG Gly	CGC Arg	TGG Trp	GAG Glu	CAT His	GGC Gly	GTC Val	CTA Leu	TAC Tyr	ATG Met	1334
			370					375					380			
AAG Lys	TAC Tyr	CCC Pro	GTG Val	TGG Trp	CCT Pro	CGC Arg	TAC Tyr	AGT Ser	GCC Ala	TCT Ser	CTG Leu	CAG Gln	CCT Pro	GTG Val	GTG Val	1382
		385					390					395				
GAC Asp	AGT Ser	CGG Arg	CAC His	CTG Leu	ACG Thr	GTG Val	GCC Ala	ACG Thr	CTG Leu	GAA Glu	GAG Glu	CGG Arg	CCC Pro	TTT Phe	GTC Val	1430
	400					405					410					
ATC Ile	GTG Val	GAG Glu	AGC Ser	CCT Pro	GAC Asp	CCT Pro	GGC Gly	ACA Thr	GGA Gly	GGC Gly	TGT Cys	GTC Val	CCC Pro	AAC Asn	ACC Thr	1478
415					420					425					430	
GTG Val	CCC Pro	TGC Cys	CGC Arg	AGG Arg	CAG Gln	AGC Ser	AAC Asn	CAC His	ACC Thr	TTC Phe	AGC Ser	AGC Ser	GGG Gly	GAC Asp	GTG Val	1526
				435					440					445		
GCC Ala	CCC Pro	TAC Tyr	ACC Thr	AAG Lys	CTC Leu	TGC Cys	TGT Cys	AAG Lys	GGA Gly	TTC Phe	TGC Cys	ATC Ile	GAC Asp	ATC Ile	CTC Leu	1574
			450					455					460			
AAG Lys	AAG Lys	CTG Leu	GCC Ala	AGA Arg	GTG Val	GTC Val	AAA Lys	TTC Phe	TCC Ser	TAC Tyr	GAC Asp	CTG Leu	TAC Tyr	CTG Leu	GTG Val	1622
		465					470					475				

ACC	AAC	GGC	AAG	CAT	GGC	AAG	CGG	GTG	CGC	GGC	GTA	TGG	AAC	GGC	ATG	1670
Thr	Asn	Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	
	480					485					490					
ATT	GGG	GAG	GTG	TAC	TAC	AAG	CGG	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	1718
Ile	Gly	Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	
495					500					505					510	
ACC	ATC	AAT	GAG	GAA	CGC	TCC	GAG	ATC	GTA	GAC	TTC	TCT	GTA	CCC	TTT	1766
Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	
				515					520					525		
GTG	GAG	ACG	GGC	ATC	AGT	GTG	ATG	GTG	GCT	CGC	AGC	AAT	GGC	ACC	GTC	1814
Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	
			530					535					540			
TCC	CCC	TCG	GCC	TTC	TTG	GAG	CCA	TAT	AGC	CCT	GCA	GTG	TGG	GTG	ATG	1862
Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	
		545					550					555				
ATG	TTT	GTC	ATG	TGC	CTC	ACT	GTG	GTG	GCC	ATC	ACC	GTC	TTC	ATG	TTC	1910
Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	
	560					565					570					
GAG	TAC	TTC	AGC	CCT	GTC	AGC	TAC	AAC	CAG	AAC	CTC	ACC	AGA	GGC	AAG	1958
Glu	Tyr	Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	
575					580					585					590	
AAG	TCC	GGG	GGC	CCA	GCT	TTC	ACT	ATC	GGC	AAG	TCC	GTG	TGG	CTG	CTG	2006
Lys	Ser	Gly	Gly	Pro	Ala	Phe	Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	
				595					600					605		
TGG	GCG	CTG	GTC	TTC	AAC	AAC	TCA	GTG	CCC	ATC	GAG	AAC	CCG	CGG	GGC	2054
Trp	Ala	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	
			610					615					620			
ACC	ACC	AGC	AAG	ATC	ATG	GTT	CTG	GTC	TGG	GCC	TTC	TTT	GCT	GTC	ATC	2102
Thr	Thr	Ser	Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	
		625					630					635				
TTC	CTC	GCC	AGA	TAC	ACG	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAA	GAG	2150
Phe	Leu	Ala	Arg	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	
	640					645						650				
CAA	TAC	ATC	GAC	ACT	GTG	TCG	GGC	CTC	AGT	GAC	AAG	AAG	TTT	CAG	CGG	2198
Gln	Tyr	Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	
655					660					665					670	
CCT	CAA	GAT	CAG	TAC	CCA	CCT	TTC	CGC	TTC	GGC	ACG	GTG	CCC	AAC	GGC	2246
Pro	Gln	Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	
				675					680					685		
AGC	ACG	GAG	CGG	AAC	ATC	CGC	AGT	AAC	TAC	CGT	GAC	ATG	CAC	ACC	CAC	2294
Ser	Thr	Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	
			690					695					700			
ATG	GTC	AAG	TTC	AAC	CAG	CGC	TCG	GTG	GAG	GAC	GCG	CTC	ACC	AGC	CTC	2342
Met	Val	Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	
		705					710					715				
AAG	ATG	GGG	AAG	CTG	GAT	GCC	TTC	ATC	TAT	GAT	GCT	GCT	GTC	CTC	AAC	2390
Lys	Met	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	
	720					725					730					
TAC	ATG	GCA	GGC	AAG	GAC	GAG	GGC	TGC	AAG	CTG	GTC	ACC	ATT	GGG	TCT	2438
Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	
735					740					745					750	

GGC Gly	AAG Lys	GTC Val	TTT Phe	GCT Ala 755	ACC Thr	ACT Thr	GGC Gly	TAC Tyr	GGC Gly 760	ATC Ile	GCC Ala	ATG Met	CAG Gln	AAG Lys 765	GAC Asp	2486
TCC Ser	CAC His	TGG Trp	AAG Lys 770	CGG Arg	GCC Ala	ATA Ile	GAC Asp	CTG Leu 775	GCG Ala	CTC Leu	TTG Leu	CAG Gln	TTC Phe 780	CTG Leu	GGG Gly	2534
GAC Asp	GGA Gly	GAG Glu 785	ACA Thr	CAG Gln	AAA Lys	CTG Leu	GAG Glu 790	ACA Thr	GTG Val	TGG Trp	CTC Leu	TCA Ser	GGG Gly 795	ATC Ile	TGC Cys	2582
CAG Gln	AAT Asn 800	GAG Glu	AAG Lys	AAC Asn	GAG Glu	GTG Val 805	ATG Met	AGC Ser	AGC Ser	AAG Lys	CTG Leu 810	GAC Asp	ATC Ile	GAC Asp	AAC Asn	2630
ATG Met 815	GCA Ala	GGC Gly	GTC Val	TTC Phe	TAC Tyr 820	ATG Met	CTG Leu	CTG Leu	GTG Val	GCC Ala 825	ATG Met	GGG Gly	CTG Leu	GCC Ala	CTG Leu 830	2678
CTG Leu	GTC Val	TTC Phe	GCC Ala	TGG Trp 835	GAG Glu	CAC His	CTG Leu	GTC Val	TAC Tyr 840	TGG Trp	AAG Lys	CTG Leu	CGC Arg	CAC His 845	TCG Ser	2726
GTG Val	CCC Pro	AAC Asn	TCA Ser 850	TCC Ser	CAG Gln	CTG Leu	GAC Asp	TTC Phe 855	CTG Leu	CTG Leu	GCT Ala	TTC Phe	AGC Ser 860	AGG Arg	GGC Gly	2774
ATC Ile	TAC Tyr	AGC Ser 865	TGC Cys	TTC Phe	AGC Ser	GGG Gly	GTG Val 870	CAG Gln	AGC Ser	CTC Leu	GCC Ala	AGC Ser 875	CCA Pro	CCG Pro	CGG Arg	2822
CAG Gln 880	GCC Ala	AGC Ser	CCG Pro	GAC Asp	CTC Leu	ACG Thr 885	GCC Ala	AGC Ser	TCG Ser	GCC Ala	CAG Gln 890	GCC Ala	AGC Ser	GTG Val	CTC Leu	2870
AAG Lys 895	ATG Met	CTG Leu	CAG Gln	GCA Ala	GCC Ala 900	CGC Arg	GAC Asp	ATG Met	GTG Val	ACC Thr 905	ACG Thr	GCG Ala	GGC Gly	GTA Val	AGC Ser 910	2918
AGC Ser	TCC Ser	CTG Leu	GAC Asp	CGC Arg 915	GCC Ala	ACT Thr	CGC Arg	ACC Thr	ATC Ile 920	GAG Glu	AAT Asn	TGG Trp	GGT Gly 925	GGC Gly	GGC Gly	2966
CGC Arg	CGT Arg	GCG Ala	CCC Pro 930	CCA Pro	CCG Pro	TCC Ser	CCC Pro	TGC Cys 935	CCG Pro	ACC Thr	CCG Pro	CGG Arg	TCT Ser 940	GGC Gly	CCC Pro	3014
AGC Ser	CCA Pro	TGC Cys 945	CTG Leu	CCC Pro	ACC Thr	CCC Pro	GAC Asp 950	CCG Pro	CCC Pro	CCA Pro	GAG Glu	CCG Pro 955	AGC Ser	CCC Pro	ACG Thr	3062
GGC Gly	TGG Trp 960	GGA Gly	CCG Pro	CCA Pro	GAC Asp	GGG Gly 965	GGT Gly	CGC Arg	GCG Ala	GCG Ala	CTT Leu 970	GTG Val	CGC Arg	AGG Arg	GCT Ala	3110
CCG Pro 975	CAG Gln	CCC Pro	CCG Pro	GGC Gly	CGC Arg 980	CCC Pro	CCG Pro	ACG Thr	CCG Pro	GGG Gly 985	CCG Pro	CCC Pro	CTG Leu	TCC Ser	GAC Asp 990	3158
GTC Val	TCC Ser	CGA Arg	GTG Val	TCG Ser 995	CGC Arg	CGC Arg	CCA Pro	GCC Ala	TGG Trp 1000	GAG Glu	GCG Ala	CGG Arg	TGG Trp	CCG Pro	GTG Val 1005	3206
CGG Arg	ACC Thr	GGG Gly	CAC His 1010	TGC Cys	GGG Gly	AGG Arg	CAC His	CTC Leu 1015	TCG Ser	GCC Ala	TCC Ser	GAG Glu	CGG Arg	CCC Pro	CTG Leu 1020	3254

TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC	3302
Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser	
1025 1030 1035	
GGC CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC	3350
Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp	
1040 1045 1050	
CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG	3398
Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu	
1055 1060 1065 1070	
CAC GCG GCC TGG GCC CGG GGC TCG CGC CCG CGT CAC GCT TCC CTG CCC	3446
His Ala Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro	
1075 1080 1085	
AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG	3494
Ser Ser Val Ala Glu Ala Phe Ala Pro Ser Ser Leu Pro Ala Gly	
1090 1095 1100	
TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGA CAC TCG GCC TGC AGG	3542
Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg	
1105 1110 1115	
CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC	3590
Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala	
1120 1125 1130	
TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG	3638
Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln	
1135 1140 1145 1150	
CAC GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTT TGC TGG GGG GCT	3686
His Val Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala	
1155 1160 1165	
GTC TGT CCT CAC CTT CCA CCC TGT GCC AGC CAC GGC TCC TGG CTC TCC	3734
Val Cys Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser	
1170 1175 1180	
GGG GCC TGG GGG CCT CTG GGG CAC AGG GGC AGG ACT CTG GGG CTG GGC	3782
Gly Ala Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly	
1185 1190 1195	
ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGG GTA GCC	3830
Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala	
1200 1205 1210	
CGT GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC	3878
Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser	
1215 1220 1225 1230	
AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA	3926
Ser Leu Glu Ser Glu Val	
1235	
GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG GCTTTTCTGG	3986
CTTCTACCAT GAAATCCTGG CCATGGGACC CCAGTGACAG ATGATGTCTT CCATGGTCAT	4046
CAGTGACCTC AGTAGCCTCA AATCATGGTG AGGGCTGGGC TTTTGCTGTC CTCTTCTCAC	4106
GCAGAGTTCT GCCAGGAGGG TGTGCTGTGG GGGTCAGACT CCTGAGGCTC TCCCTTCCCT	4166
GGGGCTAGCC AGTTACTGGT CATGCCTGCT GTGGGCATGG AGGCTGGAAC TTGTGGTTGA	4226

GGCAGGGCCA TCCCGATCCT TGCTCTACCT GGCTAGAGTT TCTTCTCATC AGAGCACTGG 4286  
 GACATTAAAC CCACCTTTTC CCAGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAG 4340

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly  
 1 5 10 15  
 Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val  
 20 25 30  
 Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val  
 35 40 45  
 Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro  
 50 55 60  
 Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln  
 65 70 75 80  
 Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu  
 85 90 95  
 Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser  
 100 105 110  
 Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val  
 115 120 125  
 Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val  
 130 135 140  
 Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr  
 145 150 155 160  
 Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala  
 165 170 175  
 Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser  
 180 185 190  
 Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro  
 195 200 205  
 Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe  
 210 215 220  
 Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala  
 225 230 235 240  
 Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn  
 245 250 255  
 Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly  
 260 265 270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys  
 275 280 285  
 Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp  
 290 295 300  
 Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His  
 305 310 315 320  
 Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu  
 325 330 335  
 Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr  
 340 345 350  
 Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu  
 355 360 365  
 Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr  
 370 375 380  
 Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser  
 385 390 395 400  
 Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val  
 405 410 415  
 Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro  
 420 425 430  
 Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro  
 435 440 445  
 Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys  
 450 455 460  
 Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn  
 465 470 475 480  
 Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly  
 485 490 495  
 Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile  
 500 505 510  
 Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu  
 515 520 525  
 Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro  
 530 535 540  
 Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe  
 545 550 555 560  
 Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr  
 565 570 575  
 Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser  
 580 585 590  
 Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala  
 595 600 605  
 Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr  
 610 615 620



Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu  
 625 630 635 640  
 Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr  
 645 650 655  
 Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln  
 660 665 670  
 Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr  
 675 680 685  
 Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val  
 690 695 700  
 Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met  
 705 710 715 720  
 Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met  
 725 730 735  
 Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys  
 740 745 750  
 Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His  
 755 760 765  
 Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly  
 770 775 780  
 Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn  
 785 790 795 800  
 Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala  
 805 810 815  
 Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val  
 820 825 830  
 Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro  
 835 840 845  
 Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr  
 850 855 860  
 Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala  
 865 870 875 880  
 Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Met  
 885 890 895  
 Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Ser Ser  
 900 905 910  
 Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly Arg Arg  
 915 920 925  
 Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro  
 930 935 940  
 Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp  
 945 950 955 960  
 Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln  
 965 970 975

Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser  
 980 985 990  
 Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr  
 995 1000 1005  
 Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro  
 1010 1015 1020  
 Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg  
 1025 1030 1035 1040  
 Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro  
 1045 1050 1055  
 Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu His Ala  
 1060 1065 1070  
 Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro Ser Ser  
 1075 1080 1085  
 Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr  
 1090 1095 1100  
 Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu  
 1105 1110 1115 1120  
 Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln  
 1125 1130 1135  
 Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val  
 1140 1145 1150  
 Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala Val Cys  
 1155 1160 1165  
 Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser Gly Ala  
 1170 1175 1180  
 Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly Thr Gly  
 1185 1190 1195 1200  
 Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala Arg Gly  
 1205 1210 1215  
 Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu  
 1220 1225 1230  
 Glu Ser Glu Val  
 1235

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

C TCT GAG GCT CAG CCT GTC CCC AG  
Ser Glu Ala Gln Pro Val Pro  
1 5

24

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Ala Gln Pro Val Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGAAGGGGGT G

11

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4808 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 311..4705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCATGGGAC CGGCTGAGCG CTGAGAATCG CGGCCGCAGC CATCAGCCCT GGAGATGACC	60
AGGAGCGGCC ACTGCTGAGA ACTATGTGGA GAGAGGCTGC GAGCCCTGCT GCAGAGCCTC	120
CGGCTGGGAT AGCCGCCCCC CGTGGGGGCG ATGCGGACAG CGCGGGACAG CCAGGGGAGC	180
GCGCTGGGGC CGCAGCATGC GGAACCCGC TAAACCCGCT GGCTGCTGAG GCGGCCGAGA	240
TGCTCGTGCG CGCAGCGCGC CCCACTGCAT CCTCGACCTT CTCGGGCTAC AGGGACCGTC	300

AGTGGCGACT	ATG	GGC	AGA	GTG	GGC	TAT	TGG	ACC	CTG	CTG	GTG	CTG	CCG			349
	Met	Gly	Arg	Val	Gly	Tyr	Trp	Thr	Leu	Leu	Val	Leu	Pro			
	1				5						10					
GCC CTT CTG GTC TGG CGC GGT CCG GCG CCG AGC GCG GCG GCG GAG AAG																397
Ala Leu Leu Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys																
	15					20					25					
GGT CCC CCC GCG CTA AAT ATT GCG GTG ATG CTG GGT CAC AGC CAC GAC																445
Gly Pro Pro Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp																
	30				35					40					45	
GTG ACA GAG CGC GAA CTT CGA ACA CTG TGG GGC CCC GAG CAG GCG GCG																493
Val Thr Glu Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala																
				50					55					60		
GGG CTG CCC CTG GAC GTG AAC GTG GTA GCT CTG CTG ATG AAC CGC ACC																541
Gly Leu Pro Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr																
			65					70					75			
GAC CCC AAG AGC CTC ATC ACG CAC GTG TGC GAC CTC ATG TCC GGG GCA																589
Asp Pro Lys Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala																
		80					85					90				
CGC ATC CAC GGC CTC GTG TTT GGG GAC GAC ACG GAC CAG GAG GCC GTA																637
Arg Ile His Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val																
	95					100					105					
GCC CAG ATG CTG GAT TTT ATC TCC TCC CAC ACC TTC GTC CCC ATC TTG																685
Ala Gln Met Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu																
	110				115					120					125	
GGC ATT CAT GGG GGC GCA TCT ATG ATC ATG GCT GAC AAG GAT CCG ACG																733
Gly Ile His Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr																
				130					135					140		
TCT ACC TTC TTC CAG TTT GGA GCG TCC ATC CAG CAG CAA GCC ACG GTC																781
Ser Thr Phe Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val																
			145				150						155			
ATG CTG AAG ATC ATG CAG GAT TAT GAC TGG CAT GTC TTC TCC CTG GTG																829
Met Leu Lys Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val																
		160					165						170			
ACC ACT ATC TTC CCT GGC TAC AGG GAA TTC ATC AGC TTC GTC AAG ACC																877
Thr Thr Ile Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr																
	175					180					185					
ACA GTG GAC AAC AGC TTT GTG GGC TGG GAC ATG CAG AAT GTG ATC ACA																925
Thr Val Asp Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr																
	190				195					200					205	
CTG GAC ACT TCC TTT GAG GAT GCA AAG ACA CAA GTC CAG CTG AAG AAG																973
Leu Asp Thr Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys																
				210				215						220		
ATC CAC TCT TCT GTC ATC TTG CTC TAC TGT TCC AAA GAC GAG GCT GTT																1021
Ile His Ser Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val																
			225				230						235			
CTC ATT CTG AGT GAG GCC CGC TCC CTT GGC CTC ACC GGG TAT GAT TTC																1069
Leu Ile Leu Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe																
		240					245					250				
TTC TGG ATT GTC CCC AGC TTG GTC TCT GGG AAC ACG GAG CTC ATC CCA																1117
Phe Trp Ile Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro																
	255					260					265					

AAA Lys 270	GAG Glu	TTT Phe	CCA Pro	TCG Ser	GGA Gly 275	CTC Leu	ATT Ile	TCT Ser	GTC Val 280	TCC Ser	TAC Tyr	GAT Asp	GAC Asp	TGG Trp 285	GAC Asp	1165
TAC Tyr	AGC Ser	CTG Leu	GAG Glu	GCG Ala 290	AGA Arg	GTG Val	AGG Arg	GAC Asp	GGC Gly 295	ATT Ile	GGC Gly	ATC Ile	CTA Leu	ACC Thr 300	ACC Thr	1213
GCT Ala	GCA Ala	TCT Ser	TCT Ser 305	ATG Met	CTG Leu	GAG Glu	AAG Lys 310	TTC Phe	TCC Ser	TAC Tyr	ATC Ile	CCC Pro	GAG Glu 315	GCC Ala	AAG Lys	1261
GCC Ala	AGC Ser	TGC Cys 320	TAC Tyr	GGG Gly	CAG Gln	ATG Met	GAG Glu 325	AGG Arg	CCA Pro	GAG Glu	GTC Val	CCG Pro 330	ATG Met	CAC His	ACC Thr	1309
TTG Leu 335	CAC His	CCA Pro	TTT Phe	ATG Met	GTC Val	AAT Asn 340	GTT Val	ACA Thr	TGG Trp	GAT Asp	GGC Gly 345	AAA Lys	GAC Asp	TTA Leu	TCC Ser	1357
TTC Phe 350	ACT Thr	GAG Glu	GAA Glu	GGC Gly 355	TAC Tyr	CAG Gln	GTG Val	CAC His	CCC Pro	AGG Arg	CTG Leu	GTG Val	GTG Val	ATT Ile	GTG Val 365	1405
CTG Leu	AAC Asn	AAA Lys	GAC Asp	CGG Arg 370	GAA Glu	TGG Trp	GAA Glu	AAG Lys	GTG Val 375	GGC Gly	AAG Lys	TGG Trp	GAG Glu	AAC Asn 380	CAT His	1453
ACG Thr	CTG Leu	AGC Ser	CTG Leu 385	AGG Arg	CAC His	GCC Ala	GTG Val	TGG Trp 390	CCC Pro	AGG Arg	TAC Tyr	AAG Lys	TCC Ser 395	TTC Phe	TCC Ser	1501
GAC Asp	TGT Cys	GAG Glu 400	CCG Pro	GAT Asp	GAC Asp	AAC Asn 405	CAT His	CTC Leu	AGC Ser	ATC Ile	GTC Val	ACC Thr 410	CTG Leu	GAG Glu	GAG Glu	1549
GCC Ala 415	CCA Pro	TTC Phe	GTC Val	ATC Ile	GTG Val	GAA Glu 420	GAC Asp	ATA Ile	GAC Asp	CCC Pro	CTG Leu 425	ACC Thr	GAG Glu	ACG Thr	TGT Cys	1597
GTG Val 430	AGG Arg	AAC Asn	ACC Thr	GTG Val	CCA Pro	TGT Cys 435	CGG Arg	AAG Lys	TTC Phe	GTC Val 440	AAA Lys	ATC Ile	AAC Asn	AAT Asn	TCA Ser 445	1645
ACC Thr	AAT Asn	GAG Glu	GGG Gly	ATG Met 450	AAT Asn	GTG Val	AAG Lys	AAA Lys	TGC Cys 455	TGC Cys	AAG Lys	GGG Gly	TTC Phe	TGC Cys 460	ATT Ile	1693
GAT Asp	ATT Ile	CTG Leu	AAG Lys 465	AAG Lys	CTT Leu	TCC Ser	AGA Arg	ACT Thr 470	GTG Val	AAG Lys	TTT Phe	ACT Thr	TAC Tyr 475	GAC Asp	CTC Leu	1741
TAT Tyr	CTG Leu	GTG Val 480	ACC Thr	AAT Asn	GGG Gly	AAG Lys	CAT His 485	GGC Gly	AAG Lys	AAA Lys	GTT Val	AAC Asn 490	AAT Asn	GTG Val	TGG Trp	1789
AAT Asn 495	GGA Gly	ATG Met	ATC Ile	GGT Gly	GAA Glu	GTG Val 500	GTC Val	TAT Tyr	CAA Gln	CGG Arg	GCA Ala 505	GTC Val	ATG Met	GCA Ala	GTT Val	1837
GGC Gly 510	TCG Ser	CTC Leu	ACC Thr	ATC Ile	AAT Asn 515	GAG Glu	GAA Glu	CGT Arg	TCT Ser	GAA Glu 520	GTG Val	GTG Val	GAC Asp	TTC Phe	TCT Ser 525	1885
GTG Val	CCC Pro	TTT Phe	GTG Val	GAA Glu 530	ACG Thr	GGA Gly	ATC Ile	AGT Ser	GTC Val 535	ATG Met	GTT Val	TCA Ser	AGA Arg	AGT Ser	AAT Asn 540	1933

GGC	ACC	GTC	TCA	CCT	TCT	GCT	TTT	CTA	GAA	CCA	TTC	AGC	GCC	TCT	GTC	1981
Gly	Thr	Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Phe	Ser	Ala	Ser	Val	
			545					550					555			
TGG	GTG	ATG	ATG	TTT	GTG	ATG	CTG	CTC	ATT	GTT	TCT	GCC	ATA	GCT	GTT	2029
Trp	Val	Met	Met	Phe	Val	Met	Leu	Leu	Ile	Val	Ser	Ala	Ile	Ala	Val	
		560					565					570				
TGG	GTC	TTG	GAT	TAC	TCC	AGC	CCT	GTT	GGA	TAC	AAC	AGA	AAC	TTA	GCC	2077
Trp	Val	Leu	Asp	Tyr	Ser		Pro	Val	Gly	Tyr	Asn	Arg	Asn	Leu	Ala	
		575				580					585					
AAA	GGG	AAA	GCA	CCC	CAT	GGG	CCT	TCT	TTT	ACA	ATT	GGA	AAA	GCT	ATA	2125
Lys	Gly	Lys	Ala	Pro	His	Gly	Pro	Ser	Phe	Thr	Ile	Gly	Lys	Ala	Ile	
590					595					600					605	
TGG	CTT	CTT	TGG	GGC	CTG	GTG	TTC	AAT	AAC	TCC	GTG	CCT	GTC	CAG	AAT	2173
Trp	Leu	Leu	Trp	Gly	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Gln	Asn	
				610					615					620		
CCT	AAA	GGG	ACC	ACC	AGC	AAG	ATC	ATG	GTA	TCT	GTA	TGG	GCC	TTC	TTC	2221
Pro	Lys	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	Ser	Val	Trp	Ala	Phe	Phe	
			625					630					635			
GCT	GTC	ATA	TTC	CTG	GCT	AGC	TAC	ACA	GCC	AAT	CTG	GCT	GCC	TTC	ATG	2269
Ala	Val	Ile	Phe	Leu	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	
		640					645					650				
ATC	CAA	GAG	GAA	TTT	GTG	GAC	CAA	GTG	ACC	GGC	CTC	AGT	GAC	AAA	AAG	2317
Ile	Gln	Glu	Glu	Phe	Val	Asp	Gln	Val	Thr	Gly	Leu	Ser	Asp	Lys	Lys	
		655				660					665					
TTT	CAG	AGA	CCT	CAT	GAC	TAT	TCC	CCA	CCT	TTT	CGA	TTT	GGG	ACA	GTG	2365
Phe	Gln	Arg	Pro	His	Asp	Tyr	Ser	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	
670					675					680					685	
CCT	AAT	GGA	AGC	ACG	GAG	AGA	AAC	ATT	CGG	AAT	AAC	TAT	CCC	TAC	ATG	2413
Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	Asn	Asn	Tyr	Pro	Tyr	Met	
				690					695					700		
CAT	CAG	TAC	ATG	ACC	AAA	TTT	AAT	CAG	AAA	GGA	GTA	GAG	GAC	GCC	TTG	2461
His	Gln	Tyr	Met	Thr	Lys	Phe	Asn	Gln	Lys	Gly	Val	Glu	Asp	Ala	Leu	
			705					710					715			
GTC	AGC	CTG	AAA	ACG	GGG	AAG	CTG	GAC	GCT	TTC	ATC	TAC	GAT	GCC	GCA	2509
Val	Ser	Leu	Lys	Thr	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	
		720					725					730				
GTC	TTG	AAT	TAC	AAG	GCT	GGG	AGG	GAT	GAA	GGC	TGC	AAG	CTG	GTG	ACC	2557
Val	Leu	Asn	Tyr	Lys	Ala	Gly	Arg	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	
		735				740					745					
ATC	GGG	AGT	GGG	TAC	ATC	TTT	GCC	ACC	ACC	GGT	TAT	GGA	ATT	GCC	CTT	2605
Ile	Gly	Ser	Gly	Tyr	Ile	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Leu	
750					755					760					765	
CAG	AAA	GGC	TCT	CCT	TGG	AAG	AGG	CAG	ATC	GAC	CTG	GCC	TTG	CTT	CAG	2653
Gln	Lys	Gly	Ser	Pro	Trp	Lys	Arg	Gln	Ile	Asp	Leu	Ala	Leu	Leu	Gln	
				770					775					780		
TTT	GTG	GGT	GAT	GGT	GAG	ATG	GAG	GAG	CTG	GAG	ACC	CTG	TGG	CTC	ACT	2701
Phe	Val	Gly	Asp	Gly	Glu	Met	Glu	Glu	Leu	Glu	Thr	Leu	Trp	Leu	Thr	
			785					790					795			
GGG	ATC	TGC	CAC	AAC	GAG	AAG	AAC	GAG	GTG	ATG	AGC	AGC	CAG	CTG	GAC	2749
Gly	Ile	Cys	His	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Gln	Leu	Asp	
		800					805						810			

ATT GAC AAC ATG GCG GGC GTA TTC TAC ATG CTG GCT GCC GCC ATG GCC Ile Asp Asn Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala 815 820 825	2797
CTT AGC CTC ATC ACC TTC ATC TGG GAG CAC CTC TTC TAC TGG AAG CTG Leu Ser Leu Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu 830 835 840 845	2845
CGC TTC TGT TTC ACG GGC GTG TGC TCC GAC CGG CCT GGG TTG CTC TTC Arg Phe Cys Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe 850 855 860	2893
TCC ATC AGC AGG GGC ATC TAC AGC TGC ATT CAT GGA GTG CAC ATT GAA Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu 865 870 875	2941
GAA AAG AAG AAG TCT CCA GAC TTC AAT CTG ACG GGA TCC CAG AGC AAC Glu Lys Lys Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn 880 885 890	2989
ATG TTA AAA CTC CTC CGG TCA GCC AAA AAC ATT TCC AGC ATG TCC AAC Met Leu Lys Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn 895 900 905	3037
ATG AAC TCC TCA AGA ATG GAC TCA CCC AAA AGA GCT GCT GAC TTC ATC Met Asn Ser Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile 910 915 920 925	3085
CAA AGA GGT TCC CTC ATC ATG GAC ATG GTT TCA GAT AAG GGG AAT TTG Gln Arg Gly Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu 930 935 940	3133
ATG TAC TCA GAC AAC AGG TCC TTT CAG GGG AAA GAG AGC ATT TTT GGA Met Tyr Ser Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly 945 950 955	3181
GAC AAC ATG AAC GAA CTC CAA ACA TTT GTG GCC AAC CGG CAG AAG GAT Asp Asn Met Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp 960 965 970	3229
AAC CTC AAT AAC TAT GTA TTC CAG GGA CAA CAT CCT CTT ACT CTC AAT Asn Leu Asn Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn 975 980 985	3277
GAG TCC AAC CCT AAC ACG GTG GAG GTG GCC GTG AGC ACA GAA TCC AAA Glu Ser Asn Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys 990 995 1000 1005	3325
GCG AAC TCT AGA CCC CGG CAG CTG TGG AAG AAA TCC GTG GAT TCC ATA Ala Asn Ser Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile 1010 1015 1020	3373
CGC CAG GAT TCA CTA TCC CAG AAT CCA GTC TCC CAG AGG GAT GAG GCA Arg Gln Asp Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala 1025 1030 1035	3421
ACA GCA GAG AAT AGG ACC CAC TCC CTA AAG AGC CCT AGG TAT CTT CCA Thr Ala Glu Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro 1040 1045 1050	3469
GAA GAG ATG GCC CAC TCT GAC ATT TCA GAA ACG TCA AAT CGG GCC ACG Glu Glu Met Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr 1055 1060 1065	3517
TGC CAC AGG GAA CCT GAC AAC AGT AAG AAC CAC AAA ACC AAG GAC AAC Cys His Arg Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn 1070 1075 1080 1085	3565

TTT AAA AGG TCA GTG GCC TCC AAA TAC CCC AAG GAC TGT AGT GAG GTC Phe Lys Arg Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val 1090 1095 1100	3613
GAG CGC ACC TAC CTG AAA ACC AAA TCA AGC TCC CCT AGA GAC AAG ATC Glu Arg Thr Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile 1105 1110 1115	3661
TAC ACT ATA GAT GGT GAG AAG GAG CCT GGT TTC CAC TTA GAT CCA CCC Tyr Thr Ile Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro 1120 1125 1130	3709
CAG TTT GTT GAA AAT GTG ACC CTG CCC GAG AAC GTG GAC TTC CCG GAC Gln Phe Val Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp 1135 1140 1145	3757
CCC TAC CAG GAT CCC AGT GAA AAC TTC CGC AAG GGG GAC TCC ACG CTG Pro Tyr Gln Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu 1150 1155 1160 1165	3805
CCA ATG AAC CGG AAC CCC TTG CAT AAT GAA GAG GGG CTT TCC AAC AAC Pro Met Asn Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn 1170 1175 1180	3853
GAC CAG TAT AAA CTC TAC TCC AAG CAC TTC ACC TTG AAA GAC AAG GGT Asp Gln Tyr Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly 1185 1190 1195	3901
TCC CCG CAC AGT GAG ACC AGC GAG CGA TAC CGG CAG AAC TCC ACG CAC Ser Pro His Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His 1200 1205 1210	3949
TGC AGA AGC TGC CTT TCC AAC ATG CCC ACC TAT TCA GGC CAC TTC ACC Cys Arg Ser Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr 1215 1220 1225	3997
ATG AGG TCC CCC TTC AAG TGC GAT GCC TGC CTG CGG ATG GGG AAC CTC Met Arg Ser Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu 1230 1235 1240 1245	4045
TAT GAC ATC GAT GAA GAC CAG ATG CTT CAG GAG ACA GGT AAC CCA GCC Tyr Asp Ile Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala 1250 1255 1260	4093
ACC GGG GAG CAG GTC TAC CAG CAG GAC TGG GCA CAG AAC AAT GCC CTT Thr Gly Glu Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu 1265 1270 1275	4141
CAA TTA CAA AAG AAC AAG CTA AGG ATT AGC CGT CAG CAT TCC TAC GAT Gln Leu Gln Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp 1280 1285 1290	4189
AAC ATT GTC GAC AAA CCT AGG GAG CTA GAC CTT AGC AGG CCC TCC CGG Asn Ile Val Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg 1295 1300 1305	4237
AGC ATA AGC CTC AAG GAC AGG GAA CGG CTT CTG GAG GGA AAT TTT TAC Ser Ile Ser Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr 1310 1315 1320 1325	4285
GGC AGC CTG TTT AGT GTC CCC TCA AGC AAA CTC TCG GGG AAA AAA AGC Gly Ser Leu Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser 1330 1335 1340	4333
TCC CTT TTC CCC CAA GGT CTG GAG GAC AGC AAG AGG AGC AAG TCT CTC Ser Leu Phe Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu 1345 1350 1355	4381



TTG CCA GAC CAC ACC TCC GAT AAC CCT TTC CTC CAC TCC CAC AGG GAT 4429  
 Leu Pro Asp His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp  
 1360 1365 1370  
 GAC CAA CGC TTG GTT ATT GGG AGA TGC CCC TCG GAC CCT TAC AAA CAC 4477  
 Asp Gln Arg Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His  
 1375 1380 1385  
 TCG TTG CCA TCC CAG GCG GTG AAT GAC AGC TAT CTT CGG TCG TCC TTG 4525  
 Ser Leu Pro Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu  
 1390 1395 1400 1405  
 AGG TCA ACG GCA TCG TAC TGT TCC AGG GAC AGT CGG GGC CAC AAT GAT 4573  
 Arg Ser Thr Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp  
 1410 1415 1420  
 GTG TAT ATT TCG GAG CAT GTT ATG CCT TAT GCT GCA AAT AAG AAT AAT 4621  
 Val Tyr Ile Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn  
 1425 1430 1435  
 ATG TAC TCT ACC CCC AGG GTT TTA AAT TCC TGC AGC AAT AGA CGC GTG 4669  
 Met Tyr Ser Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val  
 1440 1445 1450  
 TAC AAG GAA ATG CCT AGT ATC GAA TCT GAT GTT TAAAAATCTT CCATTAATGT 4722  
 Tyr Lys Glu Met Pro Ser Ile Glu Ser Asp Val 146 146  
 TTTATCTATA GGGAAATACA CGTAATGGCC AATGTTCTGG AGGGTAAATG TTGGATGTCC 4782  
 AATAGTGCCC TGCTAAGAGG AAGGAG 4808

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1464 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu  
 1 5 10 15  
 Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro  
 20 25 30  
 Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu  
 35 40 45  
 Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro  
 50 55 60  
 Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys  
 65 70 75 80  
 Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His  
 85 90 95  
 Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met  
 100 105 110  
 Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His  
 115 120 125

Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe  
 130 135 140  
 Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val Met Leu Lys  
 145 150 155 160  
 Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile  
 165 170 175  
 Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr Thr Val Asp  
 180 185 190  
 Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr Leu Asp Thr  
 195 200 205  
 Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys Ile His Ser  
 210 215 220  
 Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val Leu Ile Leu  
 225 230 235 240  
 Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe Phe Trp Ile  
 245 250 255  
 Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro Lys Glu Phe  
 260 265 270  
 Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp Tyr Ser Leu  
 275 280 285  
 Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr Ala Ala Ser  
 290 295 300  
 Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys Ala Ser Cys  
 305 310 315 320  
 Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr Leu His Pro  
 325 330 335  
 Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser Phe Thr Glu  
 340 345 350  
 Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val Leu Asn Lys  
 355 360 365  
 Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His Thr Leu Ser  
 370 375 380  
 Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser Asp Cys Glu  
 385 390 395 400  
 Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe  
 405 410 415  
 Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys Val Arg Asn  
 420 425 430  
 Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser Thr Asn Glu  
 435 440 445  
 Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu  
 450 455 460  
 Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu Tyr Leu Val  
 465 470 475 480

Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp Asn Gly Met  
 485 490 495  
 Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val Gly Ser Leu  
 500 505 510  
 Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro Phe  
 515 520 525  
 Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val  
 530 535 540  
 Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val Trp Val Met  
 545 550 555 560  
 Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val Trp Val Leu  
 565 570 575  
 Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala Lys Gly Lys  
 580 585 590  
 Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu  
 595 600 605  
 Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly  
 610 615 620  
 Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile  
 625 630 635 640  
 Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu  
 645 650 655  
 Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg  
 660 665 670  
 Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly  
 675 680 685  
 Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr  
 690 695 700  
 Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu  
 705 710 715 720  
 Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn  
 725 730 735  
 Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser  
 740 745 750  
 Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly  
 755 760 765  
 Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln Phe Val Gly  
 770 775 780  
 Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys  
 785 790 795 800  
 His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn  
 805 810 815  
 Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala Leu Ser Leu  
 820 825 830

Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys  
 835 840 845  
 Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser  
 850 855 860  
 Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys  
 865 870 875 880  
 Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys  
 885 890 895  
 Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser  
 900 905 910  
 Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly  
 915 920 925  
 Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser  
 930 935 940  
 Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met  
 945 950 955 960  
 Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn  
 965 970 975  
 Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn  
 980 985 990  
 Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser  
 995 1000 1005  
 Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp  
 1010 1015 1020  
 Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu  
 1025 1030 1035 1040  
 Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met  
 1045 1050 1055  
 Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg  
 1060 1065 1070  
 Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg  
 1075 1080 1085  
 Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr  
 1090 1095 1100  
 Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile  
 1105 1110 1115 1120  
 Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val  
 1125 1130 1135  
 Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln  
 1140 1145 1150  
 Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn  
 1155 1160 1165  
 Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr  
 1170 1175 1180

Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His  
 1185 1190 1195 1200  
 Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser  
 1205 1210 1215  
 Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser  
 1220 1225 1230  
 Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile  
 1235 1240 1245  
 Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu  
 1250 1255 1260  
 Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu Gln Leu Gln  
 1265 1270 1275 1280  
 Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val  
 1285 1290 1295  
 Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser  
 1300 1305 1310  
 Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu  
 1315 1320 1325  
 Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe  
 1330 1335 1340  
 Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp  
 1345 1350 1355 1360  
 His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg  
 1365 1370 1375  
 Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro  
 1380 1385 1390  
 Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr  
 1395 1400 1405  
 Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile  
 1410 1415 1420  
 Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser  
 1425 1430 1435 1440  
 Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu  
 1445 1450 1455  
 Met Pro Ser Ile Glu Ser Asp Val  
 1460

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGGAGGC GGCCGGCGCG GACTCTCTTC GCGGGCGCAG CGCCCCTTCC CCCTCGGACC 60  
CTCCGGTGA CATG 74

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 210..4664

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGAATTTGC ATCTCTTCAA GACACAAGAT TAAAACAAAA TTTACGCTAA ATTGGATTTT 60  
AAATTATCTT CCGTTCATTT ATCCTTCGTC TTTCTTATGT GGATATGCAA GCGAGAAGAA 120  
GGGACTGGAC ATTCCCAACA TGCTCACTCC CTTAATCTGT CCGTCTAGAG GTTTGGCTTC 180  
TACAAACCAA GGGAGTCGAC GAGTTGAAG ATG AAG CCC AGA GCG GAG TGC TGT 233  
Met Lys Pro Arg Ala Glu Cys Cys  
1 5  
TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC 281  
Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Ala Val Ser Gly Ser  
10 15 20  
AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC 329  
Arg Ala Arg Ser Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile  
25 30 35 40  
CTC GTG GGC ACT TCC GAC GAG GTG GCC ATC AAG GAT GCC CAC GAG AAA 377  
Leu Val Gly Thr Ser Asp Glu Val Ala Ile Lys Asp Ala His Glu Lys  
45 50 55  
GAT GAT TTC CAC CAT CTC TCC GTG GTA CCC CGG GTG GAA CTG GTA GCC 425  
Asp Asp Phe His His Leu Ser Val Val Pro Arg Val Glu Leu Val Ala  
60 65 70  
ATG AAT GAG ACC GAC CCA AAG AGC ATC ATC ACC CGC ATC TGT GAT CTC 473  
Met Asn Glu Thr Asp Pro Lys Ser Ile Ile Thr Arg Ile Cys Asp Leu  
75 80 85  
ATG TCT GAC CGG AAG ATC CAG GGG GTG GTG TTT GCT GAT GAC ACA GAC 521  
Met Ser Asp Arg Lys Ile Gln Gly Val Val Phe Ala Asp Asp Thr Asp  
90 95 100  
CAG GAA GCC ATC GCC CAG ATC CTC GAT TTC ATT TCA GCA CAG ACT CTC 569  
Gln Glu Ala Ile Ala Gln Ile Leu Asp Phe Ile Ser Ala Gln Thr Leu  
105 110 115 120  
ACC CCG ATC CTG GGC ATC CAC GGG GGC TCC TCT ATG ATA ATG GCA GAT 617  
Thr Pro Ile Leu Gly Ile His Gly Gly Ser Ser Met Ile Met Ala Asp  
125 130 135

AAG GAT GAA TCC TCC ATG TTC TTC CAG TTT GGC CCA TCA ATT GAA CAG Lys Asp Glu Ser Ser Met Phe Phe Gln Phe Gly Pro Ser Ile Glu Gln 140 145 150	665
CAA GCT TCC GTA ATG CTC AAC ATC ATG GAA GAA TAT GAC TGG TAC ATC Gln Ala Ser Val Met Leu Asn Ile Met Glu Glu Tyr Asp Trp Tyr Ile 155 160 165	713
TTT TCT ATC GTC ACC ACC TAT TTC CCT GGC TAC CAG GAC TTT GTA AAC Phe Ser Ile Val Thr Thr Tyr Phe Pro Gly Tyr Gln Asp Phe Val Asn 170 175 180	761
AAG ATC CGC AGC ACC ATT GAG AAT AGC TTT GTG GGC TGG GAG CTA GAG Lys Ile Arg Ser Thr Ile Glu Asn Ser Phe Val Gly Trp Glu Leu Glu 185 190 195 200	809
GAG GTC CTC CTA CTG GAC ATG TCC CTG GAC GAT GGA GAT TCT AAG ATC Glu Val Leu Leu Leu Asp Met Ser Leu Asp Asp Gly Asp Ser Lys Ile 205 210 215	857
CAG AAT CAG CTC AAG AAA CTT CAA AGC CCC ATC ATT CTT CTT TAC TGT Gln Asn Gln Leu Lys Lys Leu Gln Ser Pro Ile Ile Leu Leu Tyr Cys 220 225 230	905
ACC AAG GAA GAA GCC ACC TAC ATC TTT GAA GTG GCC AAC TCA GTA GGG Thr Lys Glu Glu Ala Thr Tyr Ile Phe Glu Val Ala Asn Ser Val Gly 235 240 245	953
CTG ACT GGC TAT GGC TAC ACG TGG ATC GTG CCC AGT CTG GTG GCA GGG Leu Thr Gly Tyr Gly Tyr Thr Trp Ile Val Pro Ser Leu Val Ala Gly 250 255 260	1001
GAT ACA GAC ACA GTG CCT GCG GAG TTC CCC ACT GGG CTC ATC TCT GTA Asp Thr Asp Thr Val Pro Ala Glu Phe Pro Thr Gly Leu Ile Ser Val 265 270 275 280	1049
TCA TAT GAT GAA TGG GAC TAT GGC CTC CCC CCC AGA GTG AGA GAT GGA Ser Tyr Asp Glu Trp Asp Tyr Gly Leu Pro Pro Arg Val Arg Asp Gly 285 290 295	1097
ATT GCC ATA ATC ACC ACT GCT GCT TCT GAC ATG CTG TCT GAG CAC AGC Ile Ala Ile Ile Thr Thr Ala Ala Ser Asp Met Leu Ser Glu His Ser 300 305 310	1145
TTC ATC CCT GAG CCC AAA AGC AGT TGT TAC AAC ACC CAC GAG AAG AGA Phe Ile Pro Glu Pro Lys Ser Ser Cys Tyr Asn Thr His Glu Lys Arg 315 320 325	1193
ATC TAC CAG TCC AAT ATG CTA AAT AGG TAT CTG ATC AAT GTC ACT TTT Ile Tyr Gln Ser Asn Met Leu Asn Arg Tyr Leu Ile Asn Val Thr Phe 330 335 340	1241
GAG GGG AGG AAT TTG TCC TTC AGT GAA GAT GGC TAC CAG ATG CAC CCG Glu Gly Arg Asn Leu Ser Phe Ser Glu Asp Gly Tyr Gln Met His Pro 345 350 355 360	1289
AAA CTG GTG ATA ATT CTT CTG AAC AAG GAG AGG AAG TGG GAA AGG GTG Lys Leu Val Ile Ile Leu Leu Asn Lys Glu Arg Lys Trp Glu Arg Val 365 370 375	1337
GGG AAG TGG AAA GAC AAG TCC CTG CAG ATG AAG TAC TAT GTG TGG CCC Gly Lys Trp Lys Asp Lys Ser Leu Gln Met Lys Tyr Tyr Val Trp Pro 380 385 390	1385
CGA ATG TGT CCA GAG ACT GAA GAG CAG GAG GAT GAC CAT CTG AGC ATT Arg Met Cys Pro Glu Thr Glu Glu Gln Glu Asp Asp His Leu Ser Ile 395 400 405	1433

GTG ACC CTG GAG GAG GCA CCA TTT GTC ATT GTG GAA AGT GTG GAC CCT Val Thr Leu Glu Glu Ala Pro Phe Val Ile Val Glu Ser Val Asp Pro 410 415 420	1481
CTG AGT GGA ACC TGC ATG AGG AAC ACA GTC CCC TGC CAA AAA CGC ATA Leu Ser Gly Thr Cys Met Arg Asn Thr Val Pro Cys Gln Lys Arg Ile 425 430 435 440	1529
GTC ACT GAG AAT AAA ACA GAC GAG GAG CCG GGT TAC ATC AAA AAA TGC Val Thr Glu Asn Lys Thr Asp Glu Glu Pro Gly Tyr Ile Lys Lys Cys 445 450 455	1577
TGC AAG GGG TTC TGT ATT GAC ATC CTT AAG AAA ATT TCT AAA TCT GTG Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys Ile Ser Lys Ser Val 460 465 470	1625
AAG TTC ACC TAT GAC CTT TAC CTG GTT ACC AAT GGC AAG CAT GGG AAG Lys Phe Thr Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys 475 480 485	1673
AAA ATC AAT GGA ACC TGG AAT GGT ATG ATT GGA GAG GTG GTC ATG AAG Lys Ile Asn Gly Thr Trp Asn Gly Met Ile Gly Glu Val Val Met Lys 490 495 500	1721
AGG GCC TAC ATG GCA GTG GGC TCA CTC ACC ATC AAT GAG GAA CGA TCG Arg Ala Tyr Met Ala Val Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser 505 510 515 520	1769
GAG GTG GTC GAC TTC TCT GTG CCC TTC ATA GAG ACA GGC ATC AGT GTC Glu Val Val Asp Phe Ser Val Pro Phe Ile Glu Thr Gly Ile Ser Val 525 530 535	1817
ATG GTG TCA CGC AGC AAT GGG ACT GTC TCA CCT TCT GCC TTC TTA GAG Met Val Ser Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu 540 545 550	1865
CCA TTC AGC GCT GAC GTA TGG GTG ATG ATG TTT GTG ATG CTG CTC ATC Pro Phe Ser Ala Asp Val Trp Val Met Met Phe Val Met Leu Leu Ile 555 560 565	1913
GTC TCA GCC GTG GCT GTC TTT GTC TTT GAG TAC TTC AGC CCT GTG GGT Val Ser Ala Val Ala Val Phe Val Phe Glu Tyr Phe Ser Pro Val Gly 570 575 580	1961
TAT AAC AGG TGC CTC GCT GAT GGC AGA GAG CCT GGT GGA CCC TCT TTC Tyr Asn Arg Cys Leu Ala Asp Gly Arg Glu Pro Gly Gly Pro Ser Phe 585 590 595 600	2009
ACC ATC GGC AAA GCT ATT TGG TTG CTC TGG GGT CTG GTG TTT AAC AAC Thr Ile Gly Lys Ala Ile Trp Leu Leu Trp Gly Leu Val Phe Asn Asn 605 610 615	2057
TCC GTA CCT GTG CAG AAC CCA AAG GGG ACC ACC TCC AAG ATC ATG GTG Ser Val Pro Val Gln Asn Pro Lys Gly Thr Thr Ser Lys Ile Met Val 620 625 630	2105
TCA GTG TGG GCC TTC TTT GCT GTC ATC TTC CTG GCC AGC TAC ACT GCC Ser Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala 635 640 645	2153
AAC TTA GCT GCC TTC ATG ATC CAA GAG GAA TAT GTG GAC CAG GTT TCT Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp Gln Val Ser 650 655 660	2201
GGC CTG AGC GAC AAA AAG TTC CAG AGA CCT AAT GAC TTC TCA CCC CCT Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Asn Asp Phe Ser Pro Pro 665 670 675 680	2249



TTC CGC TTT GGG ACC GTG CCC AAC GGC AGC ACA GAG AGA AAT ATT CGC Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg 685 690 695	2297
AAT AAC TAT GCA GAA ATG CAT GCC TAC ATG GGA AAG TTC AAC CAG AGG Asn Asn Tyr Ala Glu Met His Ala Tyr Met Gly Lys Phe Asn Gln Arg 700 705 710	2345
GGT GTA GAT GAT GCA TTG CTC TCC CTG AAA ACA GGG AAA CTG GAT GCC Gly Val Asp Asp Ala Leu Leu Ser Leu Lys Thr Gly Lys Leu Asp Ala 715 720 725	2393
TTC ATC TAT GAT GCA GCA GTG CTG AAC TAT ATG GCA GGC AGA GAT GAA Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Arg Asp Glu 730 735 740	2441
GGC TGC AAG CTG GTG ACC ATT GGC AGT GGG AAG GTC TTT GCT TCC ACT Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Ser Thr 745 750 755 760	2489
GGC TAT GGC ATT GCC ATC CAA AAA GAT TCT GGG TGG AAG CGC CAG GTG Gly Tyr Gly Ile Ala Ile Gln Lys Asp Ser Gly Trp Lys Arg Gln Val 765 770 775	2537
GAC CTT GCT ATC CTG CAG CTC TTT GGA GAT GGG GAG ATG GAA GAA CTG Asp Leu Ala Ile Leu Gln Leu Phe Gly Asp Gly Glu Met Glu Glu Leu 780 785 790	2585
GAA GCT CTC TGG CTC ACT GGC ATT TGT CAC AAT GAG AAG AAT GAG GTC Glu Ala Leu Trp Leu Thr Gly Ile Cys His Asn Glu Lys Asn Glu Val 795 800 805	2633
ATG AGC AGC CAG CTG GAC ATT GAC AAC ATG GCA GGG GTC TTC TAC ATG Met Ser Ser Gln Leu Asp Ile Asp Asn Met Ala Gly Val Phe Tyr Met 810 815 820	2681
TTG GGG GCG GCC ATG GCT CTC AGC CTC ATC ACC TTC ATC TGC GAA CAC Leu Gly Ala Ala Met Ala Leu Ser Leu Ile Thr Phe Ile Cys Glu His 825 830 835 840	2729
CTT TTC TAT TGG CAG TTC CGA CAT TGC TTT ATG GGT GTC TGT TCT GGC Leu Phe Tyr Trp Gln Phe Arg His Cys Phe Met Gly Val Cys Ser Gly 845 850 855	2777
AAG CCT GGC ATG GTC TTC TCC ATC AGC AGA GGT ATC TAC AGC TGC ATC Lys Pro Gly Met Val Phe Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile 860 865 870	2825
CAT GGG GTG GCG ATC GAG GAG CGC CAG TCT GTA ATG AAC TCC CCC ACC His Gly Val Ala Ile Glu Glu Arg Gln Ser Val Met Asn Ser Pro Thr 875 880 885	2873
GCA ACC ATG AAC AAC ACA CAC TCC AAC ATC CTG CGC CTG CTG CGC ACG Ala Thr Met Asn Asn Thr His Ser Asn Ile Leu Arg Leu Leu Arg Thr 890 895 900	2921
GCC AAG AAC ATG GCT AAC CTG TCT GGT GTG AAT GGC TCA CCG CAG AGC Ala Lys Asn Met Ala Asn Leu Ser Gly Val Asn Gly Ser Pro Gln Ser 905 910 915 920	2969
GCC CTG GAC TTC ATC CGA CGG GAG TCA TCC GTC TAT GAC ATC TCA GAG Ala Leu Asp Phe Ile Arg Arg Glu Ser Ser Val Tyr Asp Ile Ser Glu 925 930 935	3017
CAC CGC CGC AGC TTC ACG CAT TCT GAC TGC AAA TCC TAC AAC AAC CCG His Arg Arg Ser Phe Thr His Ser Asp Cys Lys Ser Tyr Asn Asn Pro 940 945 950	3065

CCC TGT GAG GAG AAC CTC TTC AGT GAC TAC ATC AGT GAG GTA GAG AGA Pro Cys Glu Glu Asn Leu Phe Ser Asp Tyr Ile Ser Glu Val Glu Arg 955 960 965	3113
ACG TTC GGG AAC CTG CAG CTG AAG GAC AGC AAC GTG TAC CAA GAT CAC Thr Phe Gly Asn Leu Gln Leu Lys Asp Ser Asn Val Tyr Gln Asp His 970 975 980	3161
TAC CAC CAT CAC CAC CGG CCC CAT AGT ATT GGC AGT GCC AGC TCC ATC Tyr His His His His Arg Pro His Ser Ile Gly Ser Ala Ser Ser Ile 985 990 995 1000	3209
GAT GGG CTC TAC GAC TGT GAC AAC CCA CCC TTC ACC ACC CAG TCC AGG Asp Gly Leu Tyr Asp Cys Asp Asn Pro Pro Phe Thr Thr Gln Ser Arg 1005 1010 1015	3257
TCC ATC AGC AAG AAG CCC CTG GAC ATC GGC CTC CCC TCC TCC AAG CAC Ser Ile Ser Lys Lys Pro Leu Asp Ile Gly Leu Pro Ser Ser Lys His 1020 1025 1030	3305
AGC CAG CTC AGT GAC CTG TAC GGC AAA TTC TCC TTC AAG AGC GAC CGC Ser Gln Leu Ser Asp Leu Tyr Gly Lys Phe Ser Phe Lys Ser Asp Arg 1035 1040 1045	3353
TAC AGT GGC CAC GAC GAC TTG ATC CGC TCC GAT GTC TCT GAC ATC TCA Tyr Ser Gly His Asp Asp Leu Ile Arg Ser Asp Val Ser Asp Ile Ser 1050 1055 1060	3401
ACC CAC ACC GTC ACC TAT GGG AAC ATC GAG GGC AAT GCC GCC AAG AGG Thr His Thr Val Thr Tyr Gly Asn Ile Glu Gly Asn Ala Ala Lys Arg 1065 1070 1075 1080	3449
CGT AAG CAG CAA TAT AAG GAC AGC CTG AAG AAG CGG CCT GCC TCG GCC Arg Lys Gln Gln Tyr Lys Asp Ser Leu Lys Lys Arg Pro Ala Ser Ala 1085 1090 1095	3497
AAG TCC CGC AGG GAG TTT GAC GAG ATC GAG CTG GCC TAC CGT CGC CGA Lys Ser Arg Arg Glu Phe Asp Glu Ile Glu Leu Ala Tyr Arg Arg Arg 1100 1105 1110	3545
CCG CCC CGC TCC CCT GAC CAC AAG CGC TAC TTC AGG GAC AAG GAA GGG Pro Pro Arg Ser Pro Asp His Lys Arg Tyr Phe Arg Asp Lys Glu Gly 1115 1120 1125	3593
CTA CGG GAC TTC TAC CTG GAC CAG TTC CGA ACA AAG GAG AAC TCA CCC Leu Arg Asp Phe Tyr Leu Asp Gln Phe Arg Thr Lys Glu Asn Ser Pro 1130 1135 1140	3641
CAC TGG GAG CAC GTA GAC CTG ACC GAC ATC TAC AAG GAG CGG AGT GAT His Trp Glu His Val Asp Leu Thr Asp Ile Tyr Lys Glu Arg Ser Asp 1145 1150 1155 1160	3689
GAC TTT AAG CGC GAC TCC ATC AGC GGA GGA GGG CCC TGT ACC AAC AGG Asp Phe Lys Arg Asp Ser Ile Ser Gly Gly Gly Pro Cys Thr Asn Arg 1165 1170 1175	3737
TCT CAC ATC AAG CAC GGG ACG GGC GAC AAA CAC GGC GTG GTC AGC GGG Ser His Ile Lys His Gly Thr Gly Asp Lys His Gly Val Val Ser Gly 1180 1185 1190	3785
GTA CCT GCA CCT TGG GAG AAG AAC CTG ACC AAC GTG GAG TGG GAG GAC Val Pro Ala Pro Trp Glu Lys Asn Leu Thr Asn Val Glu Trp Glu Asp 1195 1200 1205	3833
CGG TCC GGG GGC AAC TTC TGC CGC AGC TGT CCC TCC AAG CTG CAC AAC Arg Ser Gly Gly Asn Phe Cys Arg Ser Cys Pro Ser Lys Leu His Asn 1210 1215 1220	3881

TAC TCC ACG ACG GTG ACG GGT CAG AAC TCG GGC AGG CAG GCG TGC ATC Tyr Ser Thr Thr Val Thr Gly Gln Asn Ser Gly Arg Gln Ala Cys Ile 1225 1230 1235 1240	3929
CGG TGT GAG GCT TGC AAG AAA GCA GGC AAC CTG TAT GAC ATC AGT GAG Arg Cys Glu Ala Cys Lys Lys Ala Gly Asn Leu Tyr Asp Ile Ser Glu 1245 1250 1255	3977
GAC AAC TCC CTG CAG GAA CTG GAC CAG CCG GCT GCC CCA GTG GCG GTG Asp Asn Ser Leu Gln Glu Leu Asp Gln Pro Ala Ala Pro Val Ala Val 1260 1265 1270	4025
ACG TCA AAC GCC TCC ACC ACT AAG TAC CCT CAG AGC CCG ACT AAT TCC Thr Ser Asn Ala Ser Thr Thr Lys Tyr Pro Gln Ser Pro Thr Asn Ser 1275 1280 1285	4073
AAG GCC CAG AAG AAG AAC CGG AAC AAA CTG CGC CGG CAG CAC TCC TAC Lys Ala Gln Lys Lys Asn Arg Asn Lys Leu Arg Arg Gln His Ser Tyr 1290 1295 1300	4121
GAC ACC TTC GTG GAC CTG CAG AAG GAA GAA GCC GCC CTG GCC CCG CGC Asp Thr Phe Val Asp Leu Gln Lys Glu Glu Ala Ala Leu Ala Pro Arg 1305 1310 1315 1320	4169
AGC GTA AGC CTG AAA GAC AAG GGC CGA TTC ATG GAT GGG AGC CCC TAC Ser Val Ser Leu Lys Asp Lys Gly Arg Phe Met Asp Gly Ser Pro Tyr 1325 1330 1335	4217
GCC CAC ATG TTT GAG ATG TCA GCT GGC GAG AGC ACC TTT GCC AAC AAC Ala His Met Phe Glu Met Ser Ala Gly Glu Ser Thr Phe Ala Asn Asn 1340 1345 1350	4265
AAG TCC TCA GTG CCC ACT GCC GGA CAT CAC CAC CAC AAC AAC CCC GGC Lys Ser Ser Val Pro Thr Ala Gly His His His His Asn Asn Pro Gly 1355 1360 1365	4313
GGC GGG TAC ATG CTC AGC AAG TCG CTC TAC CCT GAC CGG GTC ACG CAA Gly Gly Tyr Met Leu Ser Lys Ser Leu Tyr Pro Asp Arg Val Thr Gln 1370 1375 1380	4361
AAC CCT TTC ATC CCC ACT TTT GGG GAC GAC CAG TGC TTG CTC CAT GGC Asn Pro Phe Ile Pro Thr Phe Gly Asp Asp Gln Cys Leu Leu His Gly 1385 1390 1395 1400	4409
AGC AAA TCC TAC TTC TTC AGG CAG CCC ACG GTG GCG GGG GCG TCG AAA Ser Lys Ser Tyr Phe Phe Arg Gln Pro Thr Val Ala Gly Ala Ser Lys 1405 1410 1415	4457
GCC AGG CCG GAC TTC CGG GCC CTT GTC ACC AAC AAG CCG GTG GTC TCG Ala Arg Pro Asp Phe Arg Ala Leu Val Thr Asn Lys Pro Val Val Ser 1420 1425 1430	4505
GCC CTT CAT GGG GCC GTG CCA GCC CGT TTC CAG AAG GAC ATC TGT ATA Ala Leu His Gly Ala Val Pro Ala Arg Phe Gln Lys Asp Ile Cys Ile 1435 1440 1445	4553
GGG AAC CAG TCC AAC CCC TGT GTG CCT AAC AAC ACA AAC CCC AGG GCT Gly Asn Gln Ser Asn Pro Cys Val Pro Asn Asn Thr Asn Pro Arg Ala 1450 1455 1460	4601
TTC AAT GGC TCC AGC AAT GGG CAT GTT TAT GAG AAA CTT TCT AGT ATT Phe Asn Gly Ser Ser Asn Gly His Val Tyr Glu Lys Leu Ser Ser Ile 1465 1470 1475 1480	4649
GAG TCT GAT GTC TGAGTGAGGG AACAGAGAGG TTAAGGTGGG TACGGGAGGG Glu Ser Asp Val	4701

TAAGGCTGTG GGTGCGTGA TGCATGTC ACGGAGGGTG ACGGGGGTGA ACTTGTTCC	4761
CATTGCTCC TTTCTGTTT TAATTTATTT ATGGGATCCT GGAGTTCTGG TTCCTACTGG	4821
GGGCAACCCT GGTGACCAGC ACCATCTCTC CTCCTTTTCA CAGTTCTCTC CTTCTTCCCC	4881
CCGCTGTCAG CCATTCTGT TCCCATGAGA TGATGCCATG GGCCCTCTCA GCAGGGGAGG	4941
GTAGAGCGGA GAAAGGAAGG GCTGCATGCG GGCTTCCTCC TGGTGTGGAA GAGCTCCTTG	5001
ATATCCTCTT TGAGTGAAGC TGGGAGAACC AAAAAGAGGC TATGTGAGCA CAAAGGTAGC	5061
TTTTCCCAA CTGATCTTTT CATTAGGTG AGGAAGCAAA AGCATCTATG TGAGACCATT	5121
TAGCACACTG CTTGTGAAAG GAAAGAGGCT CTGGCTAAAT TCATGCTGCT TAGATGACAT	5181
CTGTCTAGGA ATCATGTGCC AAGCAGAGGT TGGGAGGCCA TTTGTGTTTA TATATAAGCC	5241
CAAAAATGCT TGCTTCAACC CCATGAGACT CGATAGTGGT GGTGAACAGA ACCCAAGGTC	5301
ATTGGTGGCA GAGTGGATTC TTGAACAAAC TGGAAAGTAC GTTATGATAG TGTCCCCCGG	5361
TGCCTTGGGG ACAAGAGCAG GTGGATTGTG CGTGCATGTG TGTTTCATGCA CACTTGACAC	5421
CATGTGTAGT CAGGTGCCTC AAGAGAAGGC AACCTTGACT CTTTCGTTGA ATTTGCATCT	5481
CTTCAAGACA CAAGATTAAA ACAAATTTA CGCTAAATTG GATTTTAAAT TATCTTC	5538

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Lys	Pro	Arg	Ala	Glu	Cys	Cys	Ser	Pro	Lys	Phe	Trp	Leu	Val	Leu	1	5	10	15
Ala	Val	Leu	Ala	Val	Ser	Gly	Ser	Arg	Ala	Arg	Ser	Gln	Lys	Ser	Pro	20	25	30	
Pro	Ser	Ile	Gly	Ile	Ala	Val	Ile	Leu	Val	Gly	Thr	Ser	Asp	Glu	Val	35	40	45	
Ala	Ile	Lys	Asp	Ala	His	Glu	Lys	Asp	Asp	Phe	His	His	Leu	Ser	Val	50	55	60	
Val	Pro	Arg	Val	Glu	Leu	Val	Ala	Met	Asn	Glu	Thr	Asp	Pro	Lys	Ser	65	70	75	80
Ile	Ile	Thr	Arg	Ile	Cys	Asp	Leu	Met	Ser	Asp	Arg	Lys	Ile	Gln	Gly	85	90	95	
Val	Val	Phe	Ala	Asp	Asp	Thr	Asp	Gln	Glu	Ala	Ile	Ala	Gln	Ile	Leu	100	105	110	
Asp	Phe	Ile	Ser	Ala	Gln	Thr	Leu	Thr	Pro	Ile	Leu	Gly	Ile	His	Gly	115	120	125	
Gly	Ser	Ser	Met	Ile	Met	Ala	Asp	Lys	Asp	Glu	Ser	Ser	Met	Phe	Phe	130	135	140	

Gln Phe Gly Pro Ser Ile Glu Gln Gln Ala Ser Val Met Leu Asn Ile  
 145 150 155 160  
 Met Glu Glu Tyr Asp Trp Tyr Ile Phe Ser Ile Val Thr Thr Tyr Phe  
 165 170 175  
 Pro Gly Tyr Gln Asp Phe Val Asn Lys Ile Arg Ser Thr Ile Glu Asn  
 180 185 190  
 Ser Phe Val Gly Trp Glu Leu Glu Glu Val Leu Leu Leu Asp Met Ser  
 195 200 205  
 Leu Asp Asp Gly Asp Ser Lys Ile Gln Asn Gln Leu Lys Lys Leu Gln  
 210 215 220  
 Ser Pro Ile Ile Leu Leu Tyr Cys Thr Lys Glu Glu Ala Thr Tyr Ile  
 225 230 235 240  
 Phe Glu Val Ala Asn Ser Val Gly Leu Thr Gly Tyr Gly Tyr Thr Trp  
 245 250 255  
 Ile Val Pro Ser Leu Val Ala Gly Asp Thr Asp Thr Val Pro Ala Glu  
 260 265 270  
 Phe Pro Thr Gly Leu Ile Ser Val Ser Tyr Asp Glu Trp Asp Tyr Gly  
 275 280 285  
 Leu Pro Pro Arg Val Arg Asp Gly Ile Ala Ile Ile Thr Thr Ala Ala  
 290 295 300  
 Ser Asp Met Leu Ser Glu His Ser Phe Ile Pro Glu Pro Lys Ser Ser  
 305 310 315 320  
 Cys Tyr Asn Thr His Glu Lys Arg Ile Tyr Gln Ser Asn Met Leu Asn  
 325 330 335  
 Arg Tyr Leu Ile Asn Val Thr Phe Glu Gly Arg Asn Leu Ser Phe Ser  
 340 345 350  
 Glu Asp Gly Tyr Gln Met His Pro Lys Leu Val Ile Ile Leu Leu Asn  
 355 360 365  
 Lys Glu Arg Lys Trp Glu Arg Val Gly Lys Trp Lys Asp Lys Ser Leu  
 370 375 380  
 Gln Met Lys Tyr Tyr Val Trp Pro Arg Met Cys Pro Glu Thr Glu Glu  
 385 390 395 400  
 Gln Glu Asp Asp His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe  
 405 410 415  
 Val Ile Val Glu Ser Val Asp Pro Leu Ser Gly Thr Cys Met Arg Asn  
 420 425 430  
 Thr Val Pro Cys Gln Lys Arg Ile Val Thr Glu Asn Lys Thr Asp Glu  
 435 440 445  
 Glu Pro Gly Tyr Ile Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile  
 450 455 460  
 Leu Lys Lys Ile Ser Lys Ser Val Lys Phe Thr Tyr Asp Leu Tyr Leu  
 465 470 475 480  
 Val Thr Asn Gly Lys His Gly Lys Lys Ile Asn Gly Thr Trp Asn Gly  
 485 490 495

Met Ile Gly Glu Val Val Met Lys Arg Ala Tyr Met Ala Val Gly Ser  
 500 505 510  
 Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro  
 515 520 525  
 Phe Ile Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr  
 530 535 540  
 Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Asp Val Trp Val  
 545 550 555 560  
 Met Met Phe Val Met Leu Leu Ile Val Ser Ala Val Ala Val Phe Val  
 565 570 575  
 Phe Glu Tyr Phe Ser Pro Val Gly Tyr Asn Arg Cys Leu Ala Asp Gly  
 580 585 590  
 Arg Glu Pro Gly Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu  
 595 600 605  
 Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys  
 610 615 620  
 Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val  
 625 630 635 640  
 Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln  
 645 650 655  
 Glu Glu Tyr Val Asp Gln Val Ser Gly Leu Ser Asp Lys Lys Phe Gln  
 660 665 670  
 Arg Pro Asn Asp Phe Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn  
 675 680 685  
 Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Ala Glu Met His Ala  
 690 695 700  
 Tyr Met Gly Lys Phe Asn Gln Arg Gly Val Asp Asp Ala Leu Leu Ser  
 705 710 715 720  
 Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu  
 725 730 735  
 Asn Tyr Met Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly  
 740 745 750  
 Ser Gly Lys Val Phe Ala Ser Thr Gly Tyr Gly Ile Ala Ile Gln Lys  
 755 760 765  
 Asp Ser Gly Trp Lys Arg Gln Val Asp Leu Ala Ile Leu Gln Leu Phe  
 770 775 780  
 Gly Asp Gly Glu Met Glu Glu Leu Glu Ala Leu Trp Leu Thr Gly Ile  
 785 790 795 800  
 Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp  
 805 810 815  
 Asn Met Ala Gly Val Phe Tyr Met Leu Gly Ala Ala Met Ala Leu Ser  
 820 825 830  
 Leu Ile Thr Phe Ile Cys Glu His Leu Phe Tyr Trp Gln Phe Arg His  
 835 840 845

Cys Phe Met Gly Val Cys Ser Gly Lys Pro Gly Met Val Phe Ser Ile  
 850 855 860  
 Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val Ala Ile Glu Glu Arg  
 865 870 875 880  
 Gln Ser Val Met Asn Ser Pro Thr Ala Thr Met Asn Asn Thr His Ser  
 885 890 895  
 Asn Ile Leu Arg Leu Leu Arg Thr Ala Lys Asn Met Ala Asn Leu Ser  
 900 905 910  
 Gly Val Asn Gly Ser Pro Gln Ser Ala Leu Asp Phe Ile Arg Arg Glu  
 915 920 925  
 Ser Ser Val Tyr Asp Ile Ser Glu His Arg Arg Ser Phe Thr His Ser  
 930 935 940  
 Asp Cys Lys Ser Tyr Asn Asn Pro Pro Cys Glu Glu Asn Leu Phe Ser  
 945 950 955 960  
 Asp Tyr Ile Ser Glu Val Glu Arg Thr Phe Gly Asn Leu Gln Leu Lys  
 965 970 975  
 Asp Ser Asn Val Tyr Gln Asp His Tyr His His His His Arg Pro His  
 980 985 990  
 Ser Ile Gly Ser Ala Ser Ser Ile Asp Gly Leu Tyr Asp Cys Asp Asn  
 995 1000 1005  
 Pro Pro Phe Thr Thr Gln Ser Arg Ser Ile Ser Lys Lys Pro Leu Asp  
 1010 1015 1020  
 Ile Gly Leu Pro Ser Ser Lys His Ser Gln Leu Ser Asp Leu Tyr Gly  
 1025 1030 1035 1040  
 Lys Phe Ser Phe Lys Ser Asp Arg Tyr Ser Gly His Asp Asp Leu Ile  
 1045 1050 1055  
 Arg Ser Asp Val Ser Asp Ile Ser Thr His Thr Val Thr Tyr Gly Asn  
 1060 1065 1070  
 Ile Glu Gly Asn Ala Ala Lys Arg Arg Lys Gln Gln Tyr Lys Asp Ser  
 1075 1080 1085  
 Leu Lys Lys Arg Pro Ala Ser Ala Lys Ser Arg Arg Glu Phe Asp Glu  
 1090 1095 1100  
 Ile Glu Leu Ala Tyr Arg Arg Arg Pro Pro Arg Ser Pro Asp His Lys  
 1105 1110 1115 1120  
 Arg Tyr Phe Arg Asp Lys Glu Gly Leu Arg Asp Phe Tyr Leu Asp Gln  
 1125 1130 1135  
 Phe Arg Thr Lys Glu Asn Ser Pro His Trp Glu His Val Asp Leu Thr  
 1140 1145 1150  
 Asp Ile Tyr Lys Glu Arg Ser Asp Asp Phe Lys Arg Asp Ser Ile Ser  
 1155 1160 1165  
 Gly Gly Gly Pro Cys Thr Asn Arg Ser His Ile Lys His Gly Thr Gly  
 1170 1175 1180  
 Asp Lys His Gly Val Val Ser Gly Val Pro Ala Pro Trp Glu Lys Asn  
 1185 1190 1195 1200

Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg  
 1205 1210 1215  
 Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln  
 1220 1225 1230  
 Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Lys Ala  
 1235 1240 1245  
 Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp  
 1250 1255 1260  
 Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys  
 1265 1270 1275 1280  
 Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn  
 1285 1290 1295  
 Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys  
 1300 1305 1310  
 Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly  
 1315 1320 1325  
 Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala  
 1330 1335 1340  
 Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly  
 1345 1350 1355 1360  
 His His His His Asn Asn Pro Gly Gly Gly Tyr Met Leu Ser Lys Ser  
 1365 1370 1375  
 Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly  
 1380 1385 1390  
 Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln  
 1395 1400 1405  
 Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu  
 1410 1415 1420  
 Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala  
 1425 1430 1435 1440  
 Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val  
 1445 1450 1455  
 Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His  
 1460 1465 1470  
 Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val  
 1475 1480

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA



## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 485..4495

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGAGAACACA GCGAGTGTGT GAGTCCCTCC CGCTCCAGCT CCTCCAAGCC GCGGCCGCCG	60
CCGCCACCCT CGCCCGCAGC CTCCCGCAGC CTCCCTCGGC CACCGGTGTC TGGTGGGGGT	120
GTTGCCTGGG TAGGTCGGCC CGGCCCCCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCCGA	180
GAAACATGTG TGGCCACGTC CTCGCCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA	240
GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG	300
TCCCGGCTTG CCGTTGTGCG CACCACCACT GCCGCCGCC CGGGGCCTGC CCCCACATC	360
GGCTCTCTGA GCCCTCCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTC GGTCTGGCC	420
CCCCGCCCAT CCCCCCAACA GAACAGGGTC ATGAAAAGAG GCCGCCCGGC GGGGCCCGCA	480
GGCG ATG CGC GGC GCC GGT GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG	529
Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys	
1 5 10 15	
ATG CTG CTG CTG CTG GCG CTG GCC TGC GCC AGC CCG TTC CCG GAG GAG	577
Met Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu	
20 25 30	
GCG CCG GGG CCG GGC GGG GCC GGT GGG CCC GGC GGC GGC CTC GGC GGG	625
Ala Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly	
35 40 45	
GCG CGG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG	673
Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala	
50 55 60	
GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC	721
Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Ala Val Arg Ser	
65 70 75	
CCG GGC CTA GAC GTG CGG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC	769
Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp	
80 85 90 95	
CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGG TTG CGC	817
Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg	
100 105 110	
GTG CAC GGC GTG GTC TTC GAA GAC GAC TCG CGC GCG CCC GCC GTC GCG	865
Val His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala	
115 120 125	
CCC ATC CTC GAC TTC CTG TCG GCG CAG ACC TCG CTC CCC ATC GTG TCC	913
Pro Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser	
130 135 140	
GAG CAC GGC GGC GCC GCG CTC GTG CTC ACG CCC AAG GAG AAG GGC TCC	961
Glu His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser	
145 150 155	
ACC TTC CTC CAC CTG GGC TCT TCC CCC GAG CAA CAG CTT CAG GTC ATC	1009
Thr Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile	
160 165 170 175	

TTT GAG GTG CTG GAG GAG TAT GAC TGG ACG TCC TTT GTA GCC GTG ACC	1057
Phe Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr	
180 185 190	
ACT CGT GCC CCT GGC CAC CGG GCC TTC CTG TCC TAC ATT GAG GTG CTG	1105
Thr Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu	
195 200 205	
ACT GAC GGC AGT CTG GTG GGC TGG GAG CAC CGC GGA GCG CTG ACG CTG	1153
Thr Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu	
210 215 220	
GAC CCT GGG GCG GGC GAG GCC GTG CTC AGT GCC CAG CTC GCG AGT GTC	1201
Asp Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val	
225 230 235	
AGC GCG CAG ATC CCG CTG CTC TTC TGC GCC CGA GAG GAG GCC GAG CCC	1249
Ser Ala Gln Ile Arg Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro	
240 245 250 255	
GTG TTC CGC GCA GCT GAG GAG GCT GGC CTC ACT GGA TCT GGC TAC GTC	1297
Val Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val	
260 265 270	
TGG TTC ATG GTG GGG CCC CAG CTG GCT GGA GGC GGG GGC TCT GGG GCC	1345
Trp Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Gly Ser Gly Ala	
275 280 285	
CCT GGT GAG CCC CCT CTT CTG CCA GGA GGC GCC CCC CTG CCT GCC GGG	1393
Pro Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly	
290 295 300	
CTG TTT GCA GTG CGC TCG GCT GGC TGG CGG GAT GAC CTG GCT CGG CGA	1441
Leu Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg	
305 310 315	
GTG GCA GCT GGC GTG GCC GTA GTG GCC AGA GGT GCC CAG GCC CTG CTG	1489
Val Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu	
320 325 330 335	
CGT GAT TAT GGT TTC CTT CCT GAG CTC GGC CAC GAC TGT CGC GCC CAG	1537
Arg Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln	
340 345 350	
AAC CGC ACC CAC CGC GGG GAG AGT CTG CAT AGG TAC TTC ATG AAC ATC	1585
Asn Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile	
355 360 365	
ACG TGG GAT AAC CGG GAT TAC TCC TTC AAT GAG GAC GGC TTC CTA GTG	1633
Thr Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val	
370 375 380	
AAC CCC TCC CTG GTG GTC ATC TCC CTC ACC AGA GAC AGG ACG TGG GAG	1681
Asn Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu	
385 390 395	
GTG GTG GGC AGC TGG GAG CAG CAG ACG CTC CGC CTC AAG TAC CCG CTG	1729
Val Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu	
400 405 410 415	
TGG TCC CGC TAT GGT CGC TTC CTG CAG CCA GTG GAC GAC ACG CAG CAC	1777
Trp Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His	
420 425 430	
CTC GCG GTG GCC ACG CTG GAG GAA AGG CCG TTT GTC ATC GTG GAG CCT	1825
Leu Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro	
435 440 445	

GCA GAC CCT ATC AGC GGC ACC TGC ATC CGA GAC TCC GTC CCC TGC CGG Ala Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg 450 455 460	1873
AGC CAG CTC AAC CGA ACC CAC AGC CCT CCA CCG GAT GCC CCC CGC CCG Ser Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro 465 470 475	1921
GAA AAG CGC TGC TGC AAG GGT TTC TGC ATC GAC ATT CTG AAG CGG CTG Glu Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu 480 485 490 495	1969
GCG CAT ACC ATC GGC TTC AGC TAC GAC CTC TAC CTG GTC ACC AAT GGC Ala His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly 500 505 510	2017
AAG CAC GGA AAG AAG ATC GAT GGC GTC TGG AAC GGC ATG ATC GGG GAG Lys His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu 515 520 525	2065
GTG TTC TAC CAG CGC GCA GAC ATG GCC ATC GGC TCC CTC ACC ATC AAC Val Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn 530 535 540	2113
GAG GAG CGC TCC GAG ATC GTG GAC TTC TCC GTC CCC TTC GTG GAG ACC Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr 545 550 555	2161
GGC ATC AGC GTC ATG GTG GCG CGC AGC AAT GGC ACG GTG TCC CCC TCG Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser 560 565 570 575	2209
GCC TTC CTC GAG CCC TAC AGC CCC GCC GTG TGG GTG ATG ATG TTC GTC Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val 580 585 590	2257
ATG TGC CTC ACT GTG GTC GCC GTC ACT GTT TTC ATC TTC GAG TAC CTC Met Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu 595 600 605	2305
AGT CCT GTT GGT TAC AAC CGC AGC CTG GCC ACG GGC AAG CGC CCT GGC Ser Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly 610 615 620	2353
GGT TCA ACC TTC ACC ATT GGG AAA TCC ATC TGG CTG CTC TGG GCC CTG Gly Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu 625 630 635	2401
GTG TTC AAT AAT TCG GTG CCC GTG GAG AAC CCC CGG GGA ACC ACC AGC Val Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser 640 645 650 655	2449
AAA ATC ATG GTG CTG GTG TGG GCC TTC TTC GCC GTC ATC TTC CTC GCC Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala 660 665 670	2497
AGC TAC ACA GCC AAC CTG GCC GCC TTC ATG ATC CAG GAG GAG TAC GTG Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val 675 680 685	2545
GAT ACT GTG TCT GGG CTC AGT GAC CGC AAG TTC CAG AGG CCC CAG GAG Asp Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu 690 695 700	2593
CAG TAC CCG CCC CTG AAG TTT GGG ACC GTG CCC AAC GGC TCC ACG GAG Gln Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu 705 710 715	2641

AAG AAC ATC CGC AGC AAC TAT CCC GAC ATG CAC AGC TAC ATG GTG CGC Lys Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg 720 725 730 735	2689
TAC AAC CAG CCC CGC GTA GAG GAA GCG CTC ACT CAG CTC AAG GCA GGG Tyr Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly 740 745 750	2737
AAG CTG GAC GCC TTC ATC TAC GAT GCT GCA GTG CTC AAT TAC ATG GCC Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala 755 760 765	2785
CGC AAG GAC GAG GGC TGC AAG CTT GTC ACC ATC GGC TCC GGC AAG GTC Arg Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val 770 775 780	2833
TTC GCC ACG ACA GGC TAT GGC ATC GCC CTG CAC AAG GGC TCC CGC TGG Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp 785 790 795	2881
AAG CGG CCC ATC GAC CTG GCG TTG CTG CAG TTC CTG GGG GAT GAT GAG Lys Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu 800 805 810 815	2929
ATC GAG ATG CTG GAG CGG CTG TGG CTC TCT GGG ATC TGC CAC AAT GAC Ile Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp 820 825 830	2977
AAA ATC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC ATG GCG GGC Lys Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly 835 840 845	3025
GTC TTC TAC ATG CTC CTG GTG GCC ATG GGC CTG TCC CTG CTG GTC TTC Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe 850 855 860	3073
GCC TGG GAG CAC CTG GTG TAC TGG CGC CTG CGG CAC TGC CTG GGG CCC Ala Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro 865 870 875	3121
ACC CAC CGC ATG GAC TTC CTG CTG GCC TTC TCC AGG GGC ATG TAC AGC Thr His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser 880 885 890 895	3169
TGC TGC AGC GCT GAG GCC GCC CCA CCG CCC GCC AAG CCC CCG CCG CCG Cys Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro 900 905 910	3217
CCA CAG CCC CTG CCC AGC CCC GCG TAC CCC GCG CCG GGG CCG GCT CCC Pro Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro 915 920 925	3265
GGG CCC GCA CCT TTC GTC CCC CGC GAG CGC GCC TCA GTG GCC CGC TGG Gly Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp 930 935 940	3313
CGC CGG CCC AAG GGC GCG GGG CCG CCG GGG GGC GCG GGC CTG GCC GAC Arg Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp 945 950 955	3361
GGC TTC CAC CGC TAC TAC GGC CCC ATC GAG CCG CAG GGC CTA GGC CTC Gly Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu 960 965 970 975	3409
GGC CTG GGC GAA GCG CGC GCG GCA CCG CGG GGC GCA GCC GGG CGC CCG Gly Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro 980 985 990	3457

CTG	TCC	CCG	CCG	GCC	GCT	CAG	CCC	CCG	CAG	AAG	CCG	CCG	GCC	TCC	TAT	3505
Leu	Ser	Pro	Pro	Ala	Ala	Gln	Pro	Pro	Gln	Lys	Pro	Pro	Ala	Ser	Tyr	
			995					1000					1005			
TTC	GCC	ATC	GTA	CGC	GAC	AAG	GAG	CCA	GCC	GAG	CCC	CCC	GCC	GGC	GCC	3553
Phe	Ala	Ile	Val	Arg	Asp	Lys	Glu	Pro	Ala	Glu	Pro	Pro	Ala	Gly	Ala	
		1010					1015					1020				
TTC	CCC	GGC	TTC	CCG	TCC	CCG	CCC	GCG	CCC	CCC	GCC	GCC	GCG	GCC	ACC	3601
Phe	Pro	Gly	Phe	Pro	Ser	Pro	Pro	Ala	Pro	Pro	Ala	Ala	Ala	Ala	Thr	
	1025					1030					1035					
GCC	GTC	GGG	CCG	CCA	CTC	TGC	CGC	TTG	GCC	TTC	GAG	GAC	GAG	AGC	CCG	3649
Ala	Val	Gly	Pro	Pro	Leu	Cys	Arg	Leu	Ala	Phe	Glu	Asp	Glu	Ser	Pro	
1040					1045				1050						1055	
CCG	GCG	CCC	GCG	CGG	TGG	CCG	CGC	TCG	GAC	CCC	GAG	AGC	CAA	CCC	CTG	3697
Pro	Ala	Pro	Ala	Arg	Trp	Pro	Arg	Ser	Asp	Pro	Glu	Ser	Gln	Pro	Leu	
				1060					1065					1070		
CTG	GGG	CCA	GGC	GCG	GGC	GGC	GCG	GGG	GGC	ACG	GGG	GGC	GCA	GGC	GGA	3745
Leu	Gly	Pro	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Thr	Gly	Gly	Ala	Gly	Gly	
			1075					1080					1085			
GGA	GCC	CCG	GCC	GCT	CCG	CCC	CCG	TGC	TTC	GCC	GCG	CCG	CCC	CCG	TGC	3793
Gly	Ala	Pro	Ala	Ala	Pro	Pro	Pro	Cys	Phe	Ala	Ala	Pro	Pro	Pro	Cys	
		1090					1095					1100				
TTT	TAC	CTC	GAT	GTC	GAC	CAG	TCG	CCG	TCG	GAC	TCG	GAG	GAC	TCG	GAG	3841
Phe	Tyr	Leu	Asp	Val	Asp	Gln	Ser	Pro	Ser	Asp	Ser	Glu	Asp	Ser	Glu	
	1105					1110					1115					
AGC	CTG	GCC	GGC	GCG	TCC	CTG	GCC	GGC	CTG	GAT	CCC	TGG	TGG	TTC	GCC	3889
Ser	Leu	Ala	Gly	Ala	Ser	Leu	Ala	Gly	Leu	Asp	Pro	Trp	Trp	Phe	Ala	
1120					1125				1130						1135	
GAC	TTC	CCT	TAC	CCG	TAT	GCC	GAT	CGC	CTC	GGG	CSG	CCC	GCG	GCA	CGC	3937
Asp	Phe	Pro	Tyr	Pro	Tyr	Ala	Asp	Arg	Leu	Gly	Xaa	Pro	Ala	Ala	Arg	
				1140					1145				1150			
TAC	GGA	TTG	GTC	GAC	AAA	CTA	GGG	GGC	TGG	CTC	GCC	GGG	AGC	TGG	GAC	3985
Tyr	Gly	Leu	Val	Asp	Lys	Leu	Gly	Gly	Trp	Leu	Ala	Gly	Ser	Trp	Asp	
			1155					1160					1165			
TAC	CTG	CCT	CCS	CGC	AGC	GGT	CGG	GCC	GCC	TGG	CAC	TGT	CGG	CAC	TGC	4033
Tyr	Leu	Pro	Xaa	Arg	Ser	Gly	Arg	Ala	Ala	Trp	His	Cys	Arg	His	Cys	
		1170					1175					1180				
GCC	AGC	CTG	GAG	CTG	CTT	CCG	CCG	CCG	CGC	CAT	CTC	AGC	TGC	TCG	CAC	4081
Ala	Ser	Leu	Glu	Leu	Leu	Pro	Pro	Pro	Arg	His	Leu	Ser	Cys	Ser	His	
	1185					1190					1195					
GAT	GGC	CTG	GAC	GGC	GGC	TGG	TGG	GCG	CCA	CCG	CCT	CCA	CCC	TGG	GCC	4129
Asp	Gly	Leu	Asp	Gly	Gly	Trp	Trp	Ala	Pro	Pro	Pro	Pro	Pro	Trp	Ala	
1200					1205					1210					1215	
GCC	GGG	CCC	CTG	CCC	CGA	CGC	CGG	GCC	CGC	TGC	GGG	TGC	CCG	CGG	TCG	4177
Ala	Gly	Pro	Leu	Pro	Arg	Arg	Arg	Ala	Arg	Cys	Gly	Cys	Pro	Arg	Ser	
				1220					1225					1230		
CAC	CCG	CAC	CGC	CCG	CGG	GCC	TCG	CAC	CGC	ACG	CCC	GCC	GCT	GCC	GCG	4225
His	Pro	His	Arg	Pro	Arg	Ala	Ser	His	Arg	Thr	Pro	Ala	Ala	Ala	Ala	
			1235				1240					1245				
CCC	CAC	CAC	CAC	AGG	CAC	CGG	CGC	GCC	GCT	GGG	GGC	TGG	GAC	CTC	CCG	4273
Pro	His	His	His	Arg	His	Arg	Arg	Ala	Ala	Gly	Gly	Trp	Asp	Leu	Pro	
			1250				1255					1260				

CCG CCC GCG CCC ACC TCG CGC TCG CTC GAG GAC CTC AGC TCG TGC CCT	4321
Pro Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro	
1265 1270 1275	
CGC GCC GCC CCT GCG CGC AGG CTT ACC GGG CCC TCC CGC CAC GCT CGC	4369
Arg Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg	
1280 1285 1290 1295	
AGG TGT CCG CAC GCC GCG CAC TGG GGG CCG CCG CTG CCT ACA GCT TCC	4417
Arg Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser	
1300 1305 1310	
CAC CGG AGA CAC CGG GGC GGG GAC CTG GGC ACC CGC AGG GGC TCG GCG	4465
His Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala	
1315 1320 1325	
CAC TTC TCT AGC CTC GAG TCC GAG GTA TGACGCGGCC CCGGGGGCCC	4512
His Phe Ser Ser Leu Glu Ser Glu Val	
1330 1335	
CACCGCCCCC TTGGTCAGCG CAGGCCACGG CCCGAGGGGG CGCCCGCAGT GGACAGGACC	4572
CGCGTGGGTT GGAAGGAAA GCAGTGGAAC TGGCCGGACC CCGCCTGGAG CAGCGTCCTG	4632
CGCCCCCTGG TTCTGGAGGA ACCGCAAGCC GGAGAGGATT TGGTCCCTCA ACTATCACCC	4692
AGG	4695

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1336 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Arg	Gly	Ala	Gly	Gly	Pro	Arg	Gly	Pro	Arg	Gly	Pro	Ala	Lys	Met
1				5					10					15	
Leu	Leu	Leu	Leu	Ala	Leu	Ala	Cys	Ala	Ser	Pro	Phe	Pro	Glu	Glu	Ala
			20					25					30		
Pro	Gly	Pro	Gly	Gly	Ala	Gly	Gly	Pro	Gly	Gly	Gly	Leu	Gly	Gly	Ala
			35					40					45		
Arg	Pro	Leu	Asn	Val	Ala	Leu	Val	Phe	Ser	Gly	Pro	Ala	Tyr	Ala	Ala
		50				55					60				
Glu	Ala	Ala	Arg	Leu	Gly	Pro	Ala	Val	Ala	Ala	Ala	Val	Arg	Ser	Pro
	65				70				75						80
Gly	Leu	Asp	Val	Arg	Pro	Val	Ala	Leu	Val	Leu	Asn	Gly	Ser	Asp	Pro
				85					90					95	
Arg	Ser	Leu	Val	Leu	Gln	Leu	Cys	Asp	Leu	Leu	Ser	Gly	Leu	Arg	Val
			100					105					110		
His	Gly	Val	Val	Phe	Glu	Asp	Asp	Ser	Arg	Ala	Pro	Ala	Val	Ala	Pro
		115					120					125			
Ile	Leu	Asp	Phe	Leu	Ser	Ala	Gln	Thr	Ser	Leu	Pro	Ile	Val	Ser	Glu
	130					135					140				

His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser Thr  
 145 150 155 160  
 Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile Phe  
 165 170 175  
 Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr Thr  
 180 185 190  
 Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu Thr  
 195 200 205  
 Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu Asp  
 210 215 220  
 Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val Ser  
 225 230 235 240  
 Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro Val  
 245 250 255  
 Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val Trp  
 260 265 270  
 Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Gly Ser Gly Ala Pro  
 275 280 285  
 Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly Leu  
 290 295 300  
 Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg Val  
 305 310 315 320  
 Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu Arg  
 325 330 335  
 Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln Asn  
 340 345 350  
 Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile Thr  
 355 360 365  
 Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val Asn  
 370 375 380  
 Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu Val  
 385 390 395 400  
 Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp  
 405 410 415  
 Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu  
 420 425 430  
 Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala  
 435 440 445  
 Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser  
 450 455 460  
 Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu  
 465 470 475 480  
 Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala  
 485 490 495

His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys  
 500 505 510  
 His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val  
 515 520 525  
 Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu  
 530 535 540  
 Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly  
 545 550 555 560  
 Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala  
 565 570 575  
 Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met  
 580 585 590  
 Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser  
 595 600 605  
 Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly  
 610 615 620  
 Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val  
 625 630 635 640  
 Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys  
 645 650 655  
 Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser  
 660 665 670  
 Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp  
 675 680 685  
 Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln  
 690 695 700  
 Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys  
 705 710 715 720  
 Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr  
 725 730 735  
 Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys  
 740 745 750  
 Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg  
 755 760 765  
 Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe  
 770 775 780  
 Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp Lys  
 785 790 795 800  
 Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu Ile  
 805 810 815  
 Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp Lys  
 820 825 830  
 Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val  
 835 840 845



Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe Ala  
 850 855 860  
 Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro Thr  
 865 870 875 880  
 His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser Cys  
 885 890 895  
 Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro Pro  
 900 905 910  
 Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro Gly  
 915 920 925  
 Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp Arg  
 930 935 940  
 Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp Gly  
 945 950 955 960  
 Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu Gly  
 965 970 975  
 Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro Leu  
 980 985 990  
 Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr Phe  
 995 1000 1005  
 Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala Phe  
 1010 1015 1020  
 Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Thr Ala  
 1025 1030 1035 1040  
 Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro Pro  
 1045 1050 1055  
 Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu Leu  
 1060 1065 1070  
 Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Gly  
 1075 1080 1085  
 Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys Phe  
 1090 1095 1100  
 Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu Ser  
 1105 1110 1115 1120  
 Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala Asp  
 1125 1130 1135  
 Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg Tyr  
 1140 1145 1150  
 Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp Tyr  
 1155 1160 1165  
 Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys Ala  
 1170 1175 1180  
 Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His Asp  
 1185 1190 1195 1200

(2) INFORMATION FOR SEQ ID NO:17:

- (ii) MOLECULE TYPE: cDNA

GGGTGGCGGC CGCAGAGCAC CTCCACCATC TCCTTGTCTT ACTCCAAGAT CTGGCCCTAG 60  
TCCATGTTTG C 71

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

TGGTGGTCCC CAACCTGTAG GACTTGGTTC TGGAGGAGGA TCTGGTGTAG GCAAACATGG 60  
 ACTAGGGCCA G 71

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTTGGGGACC ACCAGATGGA GGTAGAGCTG CACTTGTACG AAGAGCTCCA CAACCACCTG 60  
 G 61

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGTGAGACGT CAGACAAAGG AGGCCCAGGT GTAGGTGGTC TACCAGGTGG TTGTGGAGCT 60  
 CT 62

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 195 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGCAGAGCA CCTCCACCAT CTCCTTGTC TACTCCAAGA TCTGGCCCTA GTCCATGTTT 60  
 GCCTACACCA GATCCTCCTC CAGAACCAAG TCCTACAGGT TGGGGACCAC CAGATGGAGG 120  
 TAGAGCTGCA CTTGTACGAA GAGCTCCACA ACCACCTGGT AGACCACCTA CACCTGGGCC 180  
 TCCTTTGTCT GACGT 195